

(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 88..129
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.8
seq AAASAVSVLLVAA/ER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

```

AABGCTTCGT AGTGGAGGAA CGGGTTTGGC GTGTGGGACG CAGCTGCCTC TGTACTGGGG      60
AGTCACGGAG TCCCGGGCTC CAGGGAC ATG GCG GCG GCC TCT GCG GTG TCG GTG      114
                               Met Ala Ala Ala Ser Ala Val Ser Val
                               -10

CTG CTG GTG GCG GCG GAG AGG AAC CGG TGG CAT CGT CTC CCG AGC CTG      162
Leu Leu Val Ala Ala Glu Arg Asn Arg Trp His Arg Leu Pro Ser Leu
-5                               1                               5                               10

CTC CTG CCG CCG AGG ACA TGG GTG TGG AGG CAA AGA ACC ATG AAG TAC      210
Leu Leu Pro Pro Arg Thr Trp Val Trp Arg Gln Arg Thr Met Lys Tyr
                               15                               20                               25

ACA ACA GCC ACA GGA AGA AAC ATG      234
Thr Thr Ala Thr Gly Arg Asn Met
                               30                               35

```

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 461 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 177..308
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.8
seq SGSGLSWARLSQS/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

```

ACTCTTTGCC ACCCTCAGAG GCGAGCTGTG GAAGCCTTGA CTCTTAGGGC CGTTTTAGAA    60
CCGGGGCCTC GGACCGGCGG GGTTCCTGCA CGTGAACCG GAACATCTGA GATGATCGSM    120
RGGCCCTGTG GAGTGTGGGG AGCGCGGGAG TTCTTTCTTC CCTCGAGGCC CGTGCC ATG    179
                                         Met
GCT TAC TCC AAA GCC AGT GGG TCC CCA GTC CTA AGC CAA GCA GTC CCG    227
Ala Tyr Ser Lys Ala Ser Gly Ser Pro Val Leu Ser Gln Ala Val Pro
      -40                      -35                      -30
GGG GAA AAC GCT TCT CAT CGC CGT GGG AGC GCG GAT CTT GGA AGT GGC    275
Gly Glu Asn Ala Ser His Arg Arg Gly Ser Ala Asp Leu Gly Ser Gly
      -25                      -20                      -15
TCT GGG CTT TCT TGG GCG AGG CTC TCA CAG AGT AGA TCG GAA ATC CAT    323
Ser Gly Leu Ser Trp Ala Arg Leu Ser Gln Ser Arg Ser Glu Ile His
      -10                      -5                      1                      5
TCT GCT GGC CCG CCC CAC CTC GGA GGA CGG ACT AAC GGA CCT GAG TTC    371
Ser Ala Gly Pro Pro His Leu Gly Gly Arg Thr Asn Gly Pro Glu Phe
              10              15              20
CCG GCC CTA TCT TAC TCT TCT CAG CTT CTC AGC TTG GCT CAG CTC AGA    419
Pro Ala Leu Ser Tyr Ser Ser Gln Leu Leu Ser Leu Ala Gln Leu Arg
              25              30              35
GGA AGA GGA ATC ACT GAA GTC TCA GAG AAG TCT CCA CTC ATC            461
Gly Arg Gly Ile Thr Glu Val Ser Glu Lys Ser Pro Leu Ile
      40              45              50

```

(2) INFORMATION FOR SEQ ID NO: 162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 175..285
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq RPVLLHLHQTAA/DE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

```

AGGCTCCGCG CTCTGGAGGC TCAGGCGCCG CGTGGGGCCC GCACCTCTGG GCAGCAGCGG    60

```

CAGCCGAGAC TCACGGTCAA GCTAAGGCGA AGAGTGGGTG GCTGAAGCCA TACTATTTTA 120

TAGAATTAAT GGRAARCMHG AAAAGMCATC ACAAACCAAG AAGAACTTTG GAAA ATG 177
Met

AAG CCT AGG AGA AAT TTA GAA GAA GAC GAT TAT TTG CAT AAG GAC ACG 225
Lys Pro Arg Arg Asn Leu Glu Glu Asp Asp Tyr Leu His Lys Asp Thr
-35 -30 -25

GGA GAG ACC AGC ATG CTA AAA AGA CCT GTG CTT TTG CAT TTG CAC CAA 273
Gly Glu Thr Ser Met Leu Lys Arg Pro Val Leu Leu His Leu His Gln
-20 -15 -10 -5

ACA GCC CAT GCT GAT GAA TTT GAC TGC CCT TCA GAA CTT CAG CAC ACA 321
Thr Ala His Ala Asp Glu Phe Asp Cys Pro Ser Glu Leu Gln His Thr
1 5 10

CAG GAA CTC TTT CCA CAG TGG CAC TTG CCA ATT AAA ATA GCT GCT ATT 369
Gln Glu Leu Phe Pro Gln Trp His Leu Pro Ile Lys Ile Ala Ala Ile
15 20 25

ATA GCA TCT CTG ACT TTT CTT TAC ACT CTT CTG AGG GAA GTA ATT CAC 417
Ile Ala Ser Leu Thr Phe Leu Tyr Thr Leu Leu Arg Glu Val Ile His
30 35 40

CCT TTA GCA ACT TCC CAT CAA CAA TAT TTT TAT AAA ATT CAA 459
Pro Leu Ala Thr Ser His Gln Gln Tyr Phe Tyr Lys Ile Gln
45 50 55

(2) INFORMATION FOR SEQ ID NO: 163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 25..81
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7
seq IPCAHLVCPTIG/DI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

AATTTGTAAG AATATTATAT ATAG ATG ATC ATC TGT TAT GAT ATT CCT TGT 51
Met Ile Ile Cys Tyr Asp Ile Pro Cys
-15

GCA CAT ATG TTG GTT TGT CCT ACT ATT GGT GAT ATT AAG TTT GAT CAC 99
Ala His Met Leu Val Cys Pro Thr Ile Gly Asp Ile Lys Phe Asp His

-10	-5	1	5	
TTG ATG AAG TGG TAT CCA TCA GAT TTC TCT ACT GAA AGG CTG				141
Leu Met Lys Trp Tyr Pro Ser Asp Phe Ser Thr Glu Arg Leu				
10	15	20		

(2) INFORMATION FOR SEQ ID NO: 164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 184..240
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7
seq STLASVPPAATFG/AD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

AACCAGGCTC TATTTAGAGC CGGGTAGGGG AGCGCAGGNC CAGATACCTC AGCGCTACCT	60
GGCGGAACTG GATTTCTCTC CCGCCTGCCG GCCTGCCTGC CACAGCCGGA CTCCGCCACT	120
CCGGTAGCCC CATGGCTGGM AACCTGTGAG ATTAGCAATA TTTTGTAGCAA CTACTTCAGT	180
GCG ATG TAC AGC TCG GAG GAC TCC ACC CTG GCC TCT GTT CCC CCT GCT	228
Met Tyr Ser Ser Glu Asp Ser Thr Leu Ala Ser Val Pro Pro Ala	
-15 -10 -5	
GCC ACC TTT GGG GCC GAT GAC TTG GTA CTG ACC CTG AGC AAC CCC CAG	276
Ala Thr Phe Gly Ala Asp Asp Leu Val Leu Thr Leu Ser Asn Pro Gln	
1 5 10	
ATG TCA TTG GAG GGT ACA GAG AAG GCC AGC TGG TTG GGG GAA CAG CCC	324
Met Ser Leu Glu Gly Thr Glu Lys Ala Ser Trp Leu Gly Glu Gln Pro	
15 20 25	
CAG TTC TGG TCG AAG ACG CAG GTT CTG GAC TGG ATC AGC TAC CAA GTG	372
Gln Phe Trp Ser Lys Thr Gln Val Leu Asp Trp Ile Ser Tyr Gln Val	
30 35 40	
GAG AAG AAC AAG TAC GAC GCG	393
Glu Lys Asn Lys Tyr Asp Ala	
45 50	

(2) INFORMATION FOR SEQ ID NO: 165:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 263 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 54..248
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.7
 seq QLEGLNWLRFWSA/QG
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

```

ACCCTGAATA CGAAGAACAT AAGCAAAGCT ACTGGAGACA CCGAGAACTA ATT ATG      56
                                     Met
                                     -65

GGG GAA GAC CCT KCC CAG CCC CGC AAG TAT AAG AAG WWG AAG AWG GAG      104
Gly Glu Asp Pro Xaa Gln Pro Arg Lys Tyr Lys Lys Xaa Lys Xaa Glu
          -60                      -55                      -50

CTA CAG GGT GAT KGG CCT CCC AGT TCT CCC ACT AAT GAT CCT ACC GTG      152
Leu Gln Gly Asp Xaa Pro Pro Ser Ser Pro Thr Asn Asp Pro Thr Val
          -45                      -40                      -35

AAA TAT GAG ACT CAG CCA CGG TTT ATC ACA GCC ACT GGA GGC ACC CTG      200
Lys Tyr Glu Thr Gln Pro Arg Phe Ile Thr Ala Thr Gly Gly Thr Leu
          -30                      -25                      -20

CAC ATG TAT CAG TTG GAA GGG CTG AAC TGG CTA CGC TTC TCC TGG GCC      248
His Met Tyr Gln Leu Glu Gly Leu Asn Trp Leu Arg Phe Ser Trp Ala
          -15                      -10                      -5

CAG GGC ACT KWC GGG
Gln Gly Thr Xaa Gly      263
  1                      5

```

(2) INFORMATION FOR SEQ ID NO: 166:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 372 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 148..273
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7
seq LLGCLQCCWLQSG/RA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

```

ACCAATTTTG TAGTTATCTG ATCTGAAGGA AGATGTGTGT GGAGGTGTTT AGTGATGTTT    60
TCCGATGACG GTGATTCCCC CTAAATCTAC GTATTAAATA CAATGAACA GGATCCACAG    120
TTCACCCCTA ATAATATAGT TTA CTGA ATG TTT TAT GTA GCT ATG ACC AAA ACT    174
                Met Phe Tyr Val Ala Met Thr Lys Thr
                -40                                -35

CAC AAA AGG ATC AGA AGC CTC TGT AAC ATC CAC CAT GGT TTG TTC CAG    222
His Lys Arg Ile Arg Ser Leu Cys Asn Ile His His Gly Leu Phe Gln
                -30                                -25                                -20

TTT ACT CAG CAG CTC CTG GGC TGT CTT CAG TGC TGT TGG CTG CAA TCA    270
Phe Thr Gln Gln Leu Leu Gly Cys Leu Gln Cys Cys Trp Leu Gln Ser
                -15                                -10                                -5

GGC AGA GCC CCA GCT ACC TAT TAC CTT GTG GAG AGT ATT GAA AAG TCA    318
Gly Arg Ala Pro Ala Thr Tyr Tyr Leu Val Glu Ser Ile Glu Lys Ser
                1                                5                                10                                15

GCA CAT GGC TCT GTA TTA NGT ACT TAT GAT CAA ACT CAG ACT CGC ATA    366
Ala His Gly Ser Val Leu Xaa Thr Tyr Asp Gln Thr Gln Thr Arg Ile
                20                                25                                30

GGC AGG    372
Gly Arg

```

(2) INFORMATION FOR SEQ ID NO: 167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 158..337
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7
seq XTCASXNPSQCLA/AF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

```

ACAGAATCTT TAGGTGGGCC TGTTGGTGAG GTCACCTTTC CCTAATGGTA TATTCCAGTT    60
CCTGTAGATC CTATTCCAGT TCCCAGGACA TATTCCAACC TCGACCTCCA GCCAACTTTG    120
AACCCTGAA GTTGTGTGCT GATGTGTTTC TAACAAC ATG GTC TCA CCC AAA GAT    175
                               Met Val Ser Pro Lys Asp
                               -60                               -55
CTT CCT CTT GTG CTT TTG CAG GAC ATT AAA GTT CCC AGC TCC ATG ACT    223
Leu Pro Leu Val Leu Leu Gln Asp Ile Lys Val Pro Ser Ser Met Thr
                               -50                               -45                               -40
GGA TCA CAT GCT GGA AAC CCT CAT ATA GAA AGG AAT GAT CTC CCC AGA    271
Gly Ser His Ala Gly Asn Pro His Ile Glu Arg Asn Asp Leu Pro Arg
                               -35                               -30                               -25
CAT GGT TCT CCT CAA TTT TTT ACA GGH HYG ACT TGT GCT TCT RCA AAC    319
His Gly Ser Pro Gln Phe Phe Thr Gly Xaa Thr Cys Ala Ser Xaa Asn
                               -20                               -15                               -10
CCA TCT CAG TGT CTG GCA GCA TTT                                343
Pro Ser Gln Cys Leu Ala Ala Phe
                               -5                                1

```

(2) INFORMATION FOR SEQ ID NO: 168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 1..45
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq FXSLFCLYFSCFL/HI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

```

ATG GAA TTT KTT TCT CTT TTC TGT CTC TAC TTC AGC TGT TTC CTA CAT    48
Met Glu Phe Xaa Ser Leu Phe Cys Leu Tyr Phe Ser Cys Phe Leu His
-15                               -10                               -5                                1
ATT ATA TAT TTT KKC AGC TGT TTC CTA TAC                                78
Ile Ile Tyr Phe Xaa Ser Cys Phe Leu Tyr
5                                10

```

(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 10..144
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq ALLELIDSPECLS/KC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

```

ACTGGAAG ATG GCG CTG CAC TTC CAG AGT TTG GCT GAA TTG GAA RTG TTA    51
  Met Ala Leu His Phe Gln Ser Leu Ala Glu Leu Glu Xaa Leu
    -45                -40                -35

TGT ACT CAT CTC TAC ATA GGG ACT GAT CTT ACA CAA AGA ATA GAG GCT    99
  Cys Thr His Leu Tyr Ile Gly Thr Asp Leu Thr Gln Arg Ile Glu Ala
    -30                -25                -20

GAG AAA GCA CTC TTG GAA CTT ATT GAC AGT CCA GAA TGT CTC AGC AAG    147
  Glu Lys Ala Leu Leu Glu Leu Ile Asp Ser Pro Glu Cys Leu Ser Lys
    -15                -10                -5                1

TGT CAA CTT TTA TTA GAA CAA GGA ACA ACA TCC TAT GCT CAG CTC CTT    195
  Cys Gln Leu Leu Leu Glu Gln Gly Thr Thr Ser Tyr Ala Gln Leu Leu
      -      5                10                15

GCA GCA ACC GKV
Ala Ala Thr Xaa
      20

```

(2) INFORMATION FOR SEQ ID NO: 170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 299..379
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.6
 seq LLLLLITPSPSPL/LF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

```

ACCTTGGGCT CCAAATTCTA GTCATAAAG ATGCAAGTKT TGCAATTTCC TATAAATGGT    60
TAAGAAAAGA GCAAGCTGTC CAGAGAGTGA GAAGTTTGAA AAGAGAGGTG CATAAGAGAG   120
AAATGATGTC CATTTGAGCC CCACCACGGA GGTATGTGG TCCCAAAGG AATGATGGCC   180
AAGCAATTAA TTTTCCTCC TAGTTCCTAG CTGCTTCTG CATTGATTGG CTTTACACAA   240
CTGGCATTTA GTCTGCATTA CACAAATAGA CACTAATTTA TTTGGAACAA GCAGCAAA   298
ATG AGA ACT TTA TTT GGT GCA GTC AGG GCT CCA TTT AGT TCC CTC ACT   346
Met Arg Thr Leu Phe Gly Ala Val Arg Ala Pro Phe Ser Ser Leu Thr
      -25                -20                -15

CTG CTT CTA ATC ACC CCT TCT CCC AGC CCT CTT CTA TTT GAT AGA GGT   394
Leu Leu Leu Ile Thr Pro Ser Pro Ser Pro Leu Leu Phe Asp Arg Gly
      -10                -5                1                5

CTG TCC CTC AGA TCA GCA ATG TCG                               418
Leu Ser Leu Arg Ser Ala Met Ser
      10
  
```

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 238 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 107..229
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.6
 seq AVSSLIAVGTSHG/LA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

```

ACACTCCTAT GATACTTCAT CTGTGGCAAG CTCAGATAGT GGTGACAGGA CCAACTTAAA    60
  
```

```

AAGGAAGAAG AAATTACCTG ATTCTTTTTC ACTTCATGGA TCAGTT ATG CGC CAT      115
                                   Met Arg His
                                   -40

TCA CTT TTG AAG GGA ATT TCT GCC CAG ATA GTG TCT GCA GCT GAC AAA      163
Ser Leu Leu Lys Gly Ile Ser Ala Gln Ile Val Ser Ala Ala Asp Lys
      -35                      -30                      -25

GTA GAT GCT GGC TTG CCT ACA GCA ATT GCA GTA TCC AGT CTG ATA GCA      211
Val Asp Ala Gly Leu Pro Thr Ala Ile Ala Val Ser Ser Leu Ile Ala
      -20                      -15                      -10

GTG GGT ACA TCT CAT GGA TTG GCT GGG                                  238
Val Gly Thr Ser His Gly Leu Ala Gly
      -5                      1

```

(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 120..164
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq LSCFIFYISSL/CF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

```

TGTGAAGATG ACAGAGATCT AACTTCTGAG AGCAGAGGTG TCAAGTGACG GTCCCCTTGG      60

AGGAATGGTC TTTGCATCTG ACTACTTCCT TCTGCAACTG TGTTCTTCCA TTAGCTTCC      119

ATG ACA CTC TCC TGC TTT ATT TTT TTC TAC ATC TCT AGC CTT TGC TGT      167
Met Thr Leu Ser Cys Phe Ile Phe Phe Tyr Ile Ser Ser Leu Cys Cys
-15                      -10                      -5                      1

TTC CTC TCC TAC CCC ACC AGG                                  188
Phe Leu Ser Tyr Pro Thr Arg
      5

```

(2) INFORMATION FOR SEQ ID NO: 173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs

- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 28..72
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq LCFLLPHHRLQEA/RQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

```

ATAGATCAGT GACGTCTTTT TCTTCAG ATG ATC CTA TGT TTC CTT CTT CCT CAT    54
                               Met Ile Leu Cys Phe Leu Leu Pro His
                               -15                      -10

CAT CGT CTT CAG GAA GCC AGA CAG ATT CAA GTA TTG AAG ATG CTG CCA    102
His Arg Leu Gln Glu Ala Arg Gln Ile Gln Val Leu Lys Met Leu Pro
   -5                      1                      5                      10

AGG GAA AAA TTA AGR AGA AGR AGA AGA GAG AAA ACA AAT AAA TGG GAA    150
Arg Glu Lys Leu Arg Arg Arg Arg Arg Glu Lys Thr Asn Lys Trp Glu
      15                      20                      25

AAA AGA AAG GGC AGC GGG
Lys Arg Lys Gly Ser Gly
      30

```

(2) INFORMATION FOR SEQ ID NO: 174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 64..105
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq FSLFALNMPLGFC/VY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

```

TTTATTTTAA CCATCTTTTA CTATTTTATAG AAGGAACTA GCTTTAGTAG TGGGTTGCCC   60
TGT ATG TTT TCT CTT TTT GCT CTT AAT ATG CCA TTG GGT TTT TGT GTG   108
  Met Phe Ser Leu Phe Ala Leu Asn Met Pro Leu Gly Phe Cys Val
                    -10                      -5                      1

TAT GTG ATT TTC AAA ATT CAT GAC TGG   135
Tyr Val Ile Phe Lys Ile His Asp Trp
                    5                      10

```

(2) INFORMATION FOR SEQ ID NO: 175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 163..255
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq SVWGVLPFPACSA/DL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

```

ATTTGATTTT AGTCAGGGTG TAAGAATATG TATTATTGTT CCCAAAAAAA TCTGTGTAAA   60
AACTTCATAG TGTGAAACAG TGGCAACTGS KTGATTAAAA CATCATTTAG AAAAGACACT   120
CTTCCCTGTT TTGAAATTGA CTCCTCAAAA GGACAGCTGA AC ATG GCC TCT TCT   174
                                     Met Ala Ser Ser
                                     -30

CCA GGT GTC GCC ATG CAC TCC CTC TGG GCC ACC ATA CAC ACT TCT GTG   222
Pro Gly Val Ala Met His Ser Leu Trp Ala Thr Ile His Thr Ser Val
    -25                      -20                      -15

TGG GGC GTG CTC CCA CCT CCA GCC TGC TCA GCT GAT CTT TTG TTC AGC   270
Trp Gly Val Leu Pro Pro Pro Ala Cys Ser Ala Asp Leu Leu Phe Ser
    -10                      -5                      1                      5

AAT GCC TGT CTA CTT CCC CAT GAG ATC CAC CTG   303
Asn Ala Cys Leu Leu Pro His Glu Ile His Leu
    10                      15

```

(2) INFORMATION FOR SEQ ID NO: 176:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 317 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Prostate
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 60..194
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.5
 seq LPRLLSLSQHSES/WI
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

```

AGAGTTTCCG GTCTGGGCTT TGGCGGGTCT GGTTTGAAGC TCTCCTGTTT GACGAAAGT      59

ATG TCT CAG GAA GGT GCG GTC CCA GCT AGC GCG GTT CCC CTG GAA GAA      107
Met Ser Gln Glu Gly Ala Val Pro Ala Ser Ala Val Pro Leu Glu Glu
-45                      -40                      -35                      -30

TTA AGT AGC TGG CCA GAG GAG CTA TGC CGC CGG GAA CTG CCG TCC GTC      155
Leu Ser Ser Trp Pro Glu Glu Leu Cys Arg Arg Glu Leu Pro Ser Val
                      -25                      -20                      -15

CTG CCC CGA CTC CTC TCA TTG TCT CAA CAT TCT GAA AGT TGG ATT GAG      203
Leu Pro Arg Leu Leu Ser Leu Ser Gln His Ser Glu Ser Trp Ile Glu
                      -10                      -5                      1

CAT ATT CAA ATT TTG AAA ATT ATT GTA GAA ATG TTT TTA CCT CAT ATG      251
His Ile Gln Ile Leu Lys Ile Ile Val Glu Met Phe Leu Pro His Met
5                      10                      15

AAC CAC CTG ACA TTG GAA CAG ACT TTC TTT TCA CAA GTG TTA CCA AAG      299
Asn His Leu Thr Leu Glu Gln Thr Phe Phe Ser Gln Val Leu Pro Lys
20                      25                      30                      35

ACT GTG AAA TTA TTC GAT      317
Thr Val Lys Leu Phe Asp
40

```

(2) INFORMATION FOR SEQ ID NO: 177:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 370 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 254..361
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq AAVVFAVVLSIHA/TV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

```

AGTAACTGTG AGGAAGGCTG CAGAGTGGCG ACGTCTACGC CGTAGGTTGG AGGCTGTGGG    60
GGGTGGCCGG GCGCCAGCTC CCAGGCCGCA GAAGTGACCT GCGGTGGAGT TCCCTCCTCG    120
CTGCTGGAGA ACGGAAGGGA ARAAGGTTSC TGGCCGGGTG AAAGTGCCTC CCTCTGCTTG    180
ACGGGGCTGA GGGGCCCGAA GTCTAGGGCG TCCGTAGTCG CCCCAGCCTC CGTGAAGCCC    240
CAGGTCTAGA GAT ATG ACC CGA GAG TGC CCA TCT CCG GCC CCG GGG CCT    289
      Met Thr Arg Glu Cys Pro Ser Pro Ala Pro Gly Pro
      -35                -30                -25

GGG GCT CCG CTG AGT GGA TCG GTG CTG GCA GAG GCG GCA GTA GTG TTT    337
Gly Ala Pro Leu Ser Gly Ser Val Leu Ala Glu Ala Ala Val Val Phe
      -20                -15                -10

GCA GTG GTG CTG AGC ATC CAC GCA ACC GTA TGG    370
Ala Val Val Leu Ser Ile His Ala Thr Val Trp
      -5                1

```

(2) INFORMATION FOR SEQ ID NO: 178:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 470 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 369..470
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 2..103
id AA059664
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 216..269

(C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 14.8
 seq LLWWALLLGLAQA/CP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

```

AAGTGGATGG TTCCAGGCAC CCTGTCTGGG GCAGGGAGGG CACAGGCCTG CACATCGAAG    60
GTGGGGTGGG ACCAGGCTGC CCCTCGCCCC AGCATCCAAG TCCTCCCTTG GCGCCCCGTG   120
GCCCTGGCAG ACTCTCAGGG CTAAGGTCCT CTGTTGCTTT TTGGTTCCAC CTTAGAAGAG   180
GCTCGCTTGA CTAAGAGTAG CTTGAAGGAG GCACC ATG CAG GAG CTG CAT CTG       233
                               Met Gln Glu Leu His Leu
                               -15

CTC TGG TGG GCG CTT CTC CTG GGC CTG GCT CAG GCC TGC CCT GAG CCC     281
Leu Trp Trp Ala Leu Leu Leu Gly Leu Ala Gln Ala Cys Pro Glu Pro
   -10                -5                      1

TGC GAC TGT GGG GAA AAG TAT GGC TTC CAG ATC GCC GAC TGT GCC TAC     329
Cys Asp Cys Gly Glu Lys Tyr Gly Phe Gln Ile Ala Asp Cys Ala Tyr
   5                10                15                20

CGC GAC CTA GAA TCC GTG CCG CCT GGC TTC CCG GCC AAT GTG ACT ACA     377
Arg Asp Leu Glu Ser Val Pro Pro Gly Phe Pro Ala Asn Val Thr Thr
                25                30                35

CTG AGC CTG TCA GCC AAC CGG CTG CCA GGC TTG CCG GAR GGT GCC TTC     425
Leu Ser Leu Ser Ala Asn Arg Leu Pro Gly Leu Pro Glu Gly Ala Phe
   40                45                50

AGG GAG GTG CCC CTG CTG CAG TCG CTG TGG CTG GCA CAC AAT GAG       470
Arg Glu Val Pro Leu Leu Gln Ser Leu Trp Leu Ala His Asn Glu
   55                60                65
  
```

(2) INFORMATION FOR SEQ ID NO: 179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 69..328
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 1..260
id H96534
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 14..67
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 13.6
seq LLLLALCATGAQG/LY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

```

CTCTCTGCGG GCG ATG GGG CGG CAG GCC CTG CTG CTT CTC GCG CTG TGC      49
      Met Gly Arg Gln Ala Leu Leu Leu Leu Ala Leu Cys
                -15                      -10

GCC ACA GGC GCC CAG GGG CTC TAC TTC CAC ATC GGC GAG ACC GAG AAG      97
Ala Thr Gly Ala Gln Gly Leu Tyr Phe His Ile Gly Glu Thr Glu Lys
      -5                1                5                10

CGC TGT TTC ATC GAG GAA ATC CCC GAC GAG ACC ATG GTC ATC GGC AAC      145
Arg Cys Phe Ile Glu Glu Ile Pro Asp Glu Thr Met Val Ile Gly Asn
                15                20                25

TAT CGT ACC CAG ATG TGG GAT AAG CAG AAG GAG GTC TTC CTG CCC TCG      193
Tyr Arg Thr Gln Met Trp Asp Lys Gln Lys Glu Val Phe Leu Pro Ser
                30                35                40

ACC CCT GGC CTG GGC ATG CAC GTG GAA GTG AAG GAC CCC GAC GGC AAG      241
Thr Pro Gly Leu Gly Met His Val Glu Val Lys Asp Pro Asp Gly Lys
                45                50                55

GTG GTG CTG TCC CGG CAG TAC GGC TCG GAG GGC CGC TTC ACG TTC ACC      289
Val Val Leu Ser Arg Gln Tyr Gly Ser Glu Gly Arg Phe Thr Phe Thr
                60                65                70

TCC CAC ABN KSG GGT GAC CAT CAA ATC TGT CTG CAC TGC GGC      331
Ser His Xaa Xaa Gly Asp His Gln Ile Cys Leu His Cys Gly
      75                80                85

```

(2) INFORMATION FOR SEQ ID NO: 180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 90..129
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..40

id AA134726
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 157..195
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 66..104
id AA134726
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 124..156
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 34..66
id AA134726
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 107..195
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 1..89
id R17226
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 76..138
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 12.7
seq ILFLLSWSGPLQG/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

```
AAGCTAACCC TCGGGCTTGA GGGGAAGAGG CTGACTGTAC GTTCCTTCTA CTCTGGCACC    60
ACTCTCCAGG CTGCC ATG GGG CCC AGC ACC CCT CTC CTC ATC TTG TTC CTT    111
      Met Gly Pro Ser Thr Pro Leu Leu Ile Leu Phe Leu
      -20                      -15                      -10

TTG TCA TGG TCG GGA CCC CTC CAA GGA CAG CAG CAC CAC CTT GTG GAG    159
Leu Ser Trp Ser Gly Pro Leu Gln Gly Gln Gln His His Leu Val Glu
      -5                      1                      5

TAC ATG GAA CGC CGA CTA GCT GCT TTA GAG GAA CGG    195
Tyr Met Glu Arg Arg Leu Ala Ala Leu Glu Glu Arg
      10                      15
```

(2) INFORMATION FOR SEQ ID NO: 181:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 352 base pairs
(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Prostate

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 313..349
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 7..43
id T67245
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 119..199
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.8
seq LLLLCPLSRGCCP/LL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

```

ACGTTACCTT TGGGTGGTGG TTTTCATTCC TGTGCCGCCT GCTTCTGGGC CAGTGATCCA   60
GGTGTCTGGT GACCACCCGG GCACAGCTGC TTGGCTGCTG TGGGCACCTC AGCTTCCC   118
ATG TCC TGT AGG GAA CTC ACC CAC CGG CCT TGC TCT CCA CAC CTC TTA   166
Met Ser Cys Arg Glu Leu Thr His Arg Pro Cys Ser Pro His Leu Leu
   -25                               -20                               -15
CTC CTG TGT CCC CTT TCT CGG GGA TGC TGC CCC CTC CTG CTG TCC KGT   214
Leu Leu Cys Pro Leu Ser Arg Gly Cys Cys Pro Leu Leu Leu Ser Xaa
   -10                               -5                               1                               5
CCY CTG TWA GGG GTG AAT CTT GAA TCC ATC TTA TCT CTT ACT CTC CCT   262
Pro Leu Xaa Gly Val Asn Leu Glu Ser Ile Leu Ser Leu Thr Leu Pro
           10                               15                               20
CCC TCT CCC AGC TCA GTC GGG CTC TCA CCC TCT GTG ACC CAS CTC ACA   310
Pro Ser Pro Ser Ser Val Gly Leu Ser Pro Ser Val Thr Xaa Leu Thr
           25                               30                               35
ACT TCA CCT GTT TCA TTG CAC TTT GCA TCC GMC CTC GCC GGG   352
Thr Ser Pro Val Ser Leu His Phe Ala Ser Xaa Leu Ala Gly
           40                               45                               50

```

(2) INFORMATION FOR SEQ ID NO: 182:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 447 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 113..306
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 71..264
 id H83784
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 42..111
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 1..70
 id H83784
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 378..414
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 346..382
 id H83784
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 305..340
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 264..299
 id H83784
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 250..350
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 2..102
 id W32197
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 392..449
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 142..199
 id W32197
 est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 349..390
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 100..141
id W32197
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 397..449
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..53
id W37255
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 85..150
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.5
seq AALLLGGLMMVVTG/DE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

AACTTGTGTC	CGGGTGGWRG	ACTGGATTAG	CTGCGGASCC	TGGAAGCTGC	CTGTCCTTCT	60
CCCTGTGCTT	AACCAGAGGT	CCCC	ATG GGT TGG ACA ATG AGG CTG GTC ACA		111	
			Met Gly Trp Thr Met Arg Leu Val Thr			
			-20	-15		
GCA GCA CTG TTA CTG GGT CTC ATG ATG GTG GTC ACT GGA GAC GAG GAT					159	
Ala Ala Leu Leu Leu Gly Leu Met Met Val Val Thr Gly Asp Glu Asp						
	-10		-5	1		
GAG AAC AGC CCG TGT GCC CAT GAG GCC CTC TTG GAC GAG GAC ACC CTC					207	
Glu Asn Ser Pro Cys Ala His Glu Ala Leu Leu Asp Glu Asp Thr Leu						
	5		10	15		
TTT TGC CAG GGC CTT GAA GTT TTC TAC CCA GAG TTG GGG AAC ATT GGC					255	
Phe Cys Gln Gly Leu Glu Val Phe Tyr Pro Glu Leu Gly Asn Ile Gly						
20		25		30	35	
TGC AAG GTT GTT CCT GAT TGT DAC AAC TAC AGA CAG AAG ATC ACC TCC					303	
Cys Lys Val Val Pro Asp Cys Xaa Asn Tyr Arg Gln Lys Ile Thr Ser						
	40		45	50		
TGG ATG GAG CCG ATA GTC AAG TTC CCG GGG GCC GTG GAC GGC GCA ACC					351	
Trp Met Glu Pro Ile Val Lys Phe Pro Gly Ala Val Asp Gly Ala Thr						
	55		60	65		
TAT ATC CTG GTG ATG GTG GAT CCA GAT GCC CCT AGC AGA GCA GAA CCC					399	
Tyr Ile Leu Val Met Val Asp Pro Asp Ala Pro Ser Arg Ala Glu Pro						
	70		75	80		
AGA CAG AGA TTC TGG AGA CAT TGG CTG GTA ACA GAT ATC AAG GGC GCC					447	
Arg Gln Arg Phe Trp Arg His Trp Leu Val Thr Asp Ile Lys Gly Ala						
85		90		95		

(2) INFORMATION FOR SEQ ID NO: 183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 125..182
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 6..63
id R18560
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 176..213
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 58..95
id R18560
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 145..182
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..38
id R13864
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 176..213
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 33..70
id R13864
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 176..213
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 2..39
id HSC01E071
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 119..190
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.3
seq VHLLSLCSGKVYA/RM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

```
ACTGGGAGCC GCCTCCGTCG CCGCCGTCAG AGCCGCCCTA TCAGAGTTCC TACCANTTTG    60
TGGTTCAGC  AGCTTCTGTT CCAGATTATC TTAACAAGAA AACCAACTGG AAAAAAAA    118
ATG AAA TTC CTT ATC TTC GCA TTT TTC GGT GGT GTT CAC CTT TTA TCC    166
Met Lys Phe Leu Ile Phe Ala Phe Phe Gly Gly Val His Leu Leu Ser
          -20                -15                -10
CTG TGC TCT GGG AAA GTA TAT GCA AGA ATG GCA TCT CTA AGA GGA CTC    214
Leu Cys Ser Gly Lys Val Tyr Ala Arg Met Ala Ser Leu Arg Gly Leu
          -5                1                5
GGG                                          217
Gly
```

(2) INFORMATION FOR SEQ ID NO: 184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 139..361
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 92..314
id AA100852
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 360..434
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 314..388
id AA100852
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 139..434
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 100..395
id AA224847
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 139..361
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 92..314
id AA161042
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 368..434
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 323..389
id AA161042
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 139..365
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 87..313
id H64488
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 52..144
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 1..93
id H64488
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 171..396
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 129..354
id AA088770
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 167..253
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.1
seq LIFLCGAALLAVG/IW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

```

AAAAAGCGCC TACCCTGCCT GCAGGTGAGC AGTGGTGTGT GAGAGCCAGG CGTCCCTCTG   60
CCTGCCCCACT CAGTGGCAAC ACCCGGGGAGC TGTTTTGTCC TTTGTGGAGC CTCAGCAGTT  120
CCCTCTTTCA GAACTYRVYK GCCAAGAGCC CTGAACAGGA GCCACC ATG CAG TGC   175
                                   Met Gln Cys
TTC AGC TTC ATT AAG ACC ATG ATG ATC CTC TTC AAT TTG CTC ATC TTT   223
Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu Leu Ile Phe
   -25                               -20                               -15
CTG TGT GGT GCA GCC CTG TTG GCA GTG GGC ATC TGG GTG TCA ATC GAT   271
Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val Ser Ile Asp
  -10                               -5                               1                               5
GGG GCA TCC TTT CTG AAG ATC TTC GGG CCA CTG TCG TCC AGT GCC ATG   319
Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser Ser Ala Met
              10                               15                               20
CAG TTT GTC AAC GTG GGC TAC TTC CTC ATC GCA GCC GGC GTT GTG GTC   367
Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly Val Val Val
              25                               30                               35
TTT GCT CTT GGT TTC CTG GGC TGC TAT GGT GCT AAG ACT GAG AGC AAG   415
Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr Glu Ser Lys
              40                               45                               50
TGT GCC CTC GTG ACG TTC                                           433
Cys Ala Leu Val Thr Phe
   55                               60

```

(2) INFORMATION FOR SEQ ID NO: 185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 128..242
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 1..115
id R58075
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 220..303

(C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.6
 seq IVSLLGFVATVTL/IP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

```

AAGATAGGCG GGTGCAGCGG GGCAGAACAT AGGTTGCCTT AGAGAGGTC CCCGGAGTCC   60
CGACGGCGGC TCAAGTCAGA GTTGCTGGGT TTTGCTCAGA TTGGTGTGGG AAGAGCCTGC  120
CTGTGGGGAG CGGCCACTCC ATACTGCTGA GGCCTCAGGA CTGCTGCTCA GCTTGCCCGT  180
TACCTGAAGA GCGGCGGAS GGGCCCCTGA CCGGTCACC ATG TGG GCC TTC TCG      234
                               Met Trp Ala Phe Ser
                               -25

GAA TTG CCC ATG CCG CTG CTG ATC AAT TTG ATC GTC TCG CTG CTG GGA      282
Glu Leu Pro Met Pro Leu Leu Ile Asn Leu Ile Val Ser Leu Leu Gly
          -20                      -15                      -10

TTT GTG GCC ACA GTC ACC CTC ATC CCG GCC TTC CGG GGC CAC TTC ATT      330
Phe Val Ala Thr Val Thr Leu Ile Pro Ala Phe Arg Gly His Phe Ile
          -5                      1                      5

GCT GCG CGC CTC TGT GGT CAG GAC CTC AAC AAA ACC AGC CAG              372
Ala Ala Arg Leu Cys Gly Gln Asp Leu Asn Lys Thr Ser Gln
  10                      15                      20
  
```

(2) INFORMATION FOR SEQ ID NO: 186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 112..403
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 33..324
id H97426
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 59..295
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 2..238
id W44834

est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 106..156
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 4..54
 id R57989
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 161..190
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 93
 region 62..91
 id R57989
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 148..204
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.3
 seq VLMRLVASAYSIA/QK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

```

AGCTGAGGTA GGGATGCSAT CCTTCTCAAA AGACTTATTG ACAGTGCCAA AGCTSGGTAC   60
TGGACACAAC GAGGGACCTG GGTCTACGAT AACGCGCTTK TGCTCCTCCT GAAGTGTCTT   120
TGGTCCAACG TTGTTCCAGA GTGTACC ATG GCT TCC AGT AAC ACT GTG TTG ATG   174
                               Met Ala Ser Ser Asn Thr Val Leu Met
                               -15

CGG TTG GTA GCC TCC GCA TAT TCT ATT GCT CAA AAG GCA GGD ATG ATA   222
Arg Leu Val Ala Ser Ala Tyr Ser Ile Ala Gln Lys Ala Gly Met Ile
-10                               -5                               1                               5

GTC AGA CGT GTT ATT GCT GAA GGA GAC CTG GGT ATT GTG GAG ADG ACC   270
Val Arg Arg Val Ile Ala Glu Gly Asp Leu Gly Ile Val Glu Xaa Thr
          10                               15                               20

TGT GCA ACA GAC CTG CAG ACC AAA GCT GAC CGA TTG GCA CAG ATG AGN   318
Cys Ala Thr Asp Leu Gln Thr Lys Ala Asp Arg Leu Ala Gln Met Xaa
          25                               30                               35

ATA TGT TCT TCA TTG GCC CGG AAA TTC CCC AAA CTC ACA ATT ATA GGG   366
Ile Cys Ser Ser Leu Ala Arg Lys Phe Pro Lys Leu Thr Ile Ile Gly
          40                               45                               50

GAA GAG GAT CTG CCT TCT RMG GAA GTG GAT CAA GAG   402
Glu Glu Asp Leu Pro Ser Xaa Glu Val Asp Gln Glu
          55                               60                               65

```

(2) INFORMATION FOR SEQ ID NO: 187:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 317 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 111..318
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 6..213
 id R18560
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 131..318
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 1..188
 id R13864
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 162..318
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 1..157
 id HSC01E071
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 207..318
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 1..112
 id AA016124
 est
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 105..176
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.9
 seq VHLLSLCSGKAIC/KN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

AAGTAAGGCT AGGYCGCGAG CTTAGTCCTG GGAGCCGCCT CCGTCGCCGC CGTCAGAGCC . 60

```

GCCCTATCAG ATTATCTTAA CAAGAAAACC AACTGGAAAA AAAA ATG AAA TTC CTT      116
                                   Met Lys Phe Leu

ATC TTC GCA TTT TTC GGT GGT GTT CAC CTT TTA TCC CTG TGC TCT GGG      164
Ile Phe Ala Phe Phe Gly Gly Val His Leu Leu Ser Leu Cys Ser Gly
-20                               -15                -10                -5

AAA GCT ATA TGC AAG AAT GGC ATC TCT AAG AGG ACT TTT GAA GAA ATA      212
Lys Ala Ile Cys Lys Asn Gly Ile Ser Lys Arg Thr Phe Glu Glu Ile
                               1                 5                 10

AAA GAA GAA ATA GCC AGC TGT GGA GAT GTT GCT AAA GCA ATC ATC AAC      260
Lys Glu Glu Ile Ala Ser Cys Gly Asp Val Ala Lys Ala Ile Ile Asn
                               15                20                25

CTA GCT GTT TAT GGT AAA GCC CAG AAC AGA TCC TAT GMG CGA TTG GCA      308
Leu Ala Val Tyr Gly Lys Ala Gln Asn Arg Ser Tyr Xaa Arg Leu Ala
                               30                35                40

CTT CTG GTT                                                              317
Leu Leu Val
45

```

(2) INFORMATION FOR SEQ ID NO: 188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 160..401
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 59..300
id H29377
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 454..499
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 356..401
id H29377
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 136..179
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 95
region 36..79
id H29377
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 397..436
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 297..336
id H29377
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 135..295
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 293..453
id N28905
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 45..127
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 4..86
id N28905
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 334..388
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 489..543
id N28905
est

-(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 135..395
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 81..341
id H11885
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 160..384
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 105..329
id H15231
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 136..181
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 93
 region 82..127
 id H15231
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 146..298
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.9
 seq ALXVLPLLGLHEA/AS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

```

AACTTCCGGG TTCGGCAATA ACCTGGAGCC GCGGCGTAG GTTGGCTCTT TAGGGCTTCA    60
CCCCGAAGCT CCACCTTCGC TCCCGTCTTT CTGGAACAC CGCTTTGATC TCGGCGGTGC    120
GGGACAGACG CTAGTGTGAG CCNMC ATG GCA GAT ACG ACC CCG AAC GGC CCC    172
                        Met Ala Asp Thr Thr Pro Asn Gly Pro
                        -50                               -45
CAA GGG GCG GGC GCT GTG CAA TTC ATG ATG ACC AAT AAA CTG GAC ACG    220
Gln Gly Ala Gly Ala Val Gln Phe Met Met Thr Asn Lys Leu Asp Thr
      -40                               -35                               -30
GCA ATG TGG CTT TCT CGC TTG TTC ACA GTT TAC TGC TCT GCT CTG NNT    268
Ala Met Trp Leu Ser Arg Leu Phe Thr Val Tyr Cys Ser Ala Leu Xaa
      -25                               -20                               -15
GTT CTG CCT CTT CTT GGG TTG CAT GAA GCA GCA AGC TTT TAC CAA CGT    316
Val Leu Pro Leu Leu Gly Leu His Glu Ala Ala Ser Phe Tyr Gln Arg
      -10                               -5                               1                               5
GCT TTG CTG GCA AAT GCT CTT ACC AGT GCT CTG AGG CTG CAT CAA AGA    364
Ala Leu Leu Ala Asn Ala Leu Thr Ser Ala Leu Arg Leu His Gln Arg
              10                               15                               20
TTA CCA CAC TTC CAG TTA AGC AGA GCA TTC CTG GCC CAG GCT TTG TTA    412
Leu Pro His Phe Gln Leu Ser Arg Ala Phe Leu Ala Gln Ala Leu Leu
              25                               30                               35
GAG GAC AGC TGC CAC TAC CTG TTG TAT TCA CTC ATC TTT GTA AAT TCC    460
Glu Asp Ser Cys His Tyr Leu Leu Tyr Ser Leu Ile Phe Val Asn Ser
              40                               45                               50
TAT CCA GTT ACA ATG AGT ATC TTC CCA GTC TTG TTA TTC    499
Tyr Pro Val Thr Met Ser Ile Phe Pro Val Leu Leu Phe
              55                               60                               65

```

(2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 45..221

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93
region 1..177
id HUMHBC4659
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 63..221

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 94
region 1..159
id AA160569
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 124..159

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97
region 97..132
id R88362
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 1..72

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.5
seq XVLVLSVVXXAMA/AF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

ATG CGT TTC CGC CAT TTT TGM AAA TWA ATT GGG MAG GTA CTG GTT TTA	48
Met Arg Phe Arg His Phe Xaa Lys Xaa Ile Gly Xaa Val Leu Val Leu	
-20 -15 -10	
AGT GTA GTT SCC GMC GCA ATG GCA GCC TTT GCA GTG SHA CCT CAG GGG	96
Ser Val Val Xaa Xaa Ala Met Ala Ala Phe Ala Val Xaa Pro Gln Gly	
-5 1 5	
CCC GCG TTA SSM TCT GAA CCA MTG MTG CYG GGT TCA CCC ACA TCT CCA	144
Pro Ala Leu Xaa Ser Glu Pro Xaa Xaa Xaa Gly Ser Pro Thr Ser Pro	
10 15 20	
AAG CCA GGA GTT AAT GCC CAG TTC TTA CCT GGA TTT TTA ATG GGG GMT	192
Lys Pro Gly Val Asn Ala Gln Phe Leu Pro Gly Phe Leu Met Gly Xaa	
25 30 35 40	

TTG CCA GCT CCG GTG ACT CCA CAA CCT
Leu Pro Ala Pro Val Thr Pro Gln Pro
45

219

(2) INFORMATION FOR SEQ ID NO: 190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 105..414
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..310
id T26956
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 45..359
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..315
id T31666
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 202..332
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 137..267
id R14990
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 127..201
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 63..137
id R14990
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 65..114
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 1..50
id R14990
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 1..120
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.2
seq LCVEFASVASCDA/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

ATG GAG TTG GGG AGT TGC CTG GAG GGC GGG AGG GAG GCG GCG GAG GAA	48
Met Glu Leu Gly Ser Cys Leu Glu Gly Gly Arg Glu Ala Ala Glu Glu	
-40 -35 -30 -25	
GAG GGC GAG CCT GAG GTG AAA AAG CGG CGA CTT CTG TGT GTG GAG TTT	96
Glu Gly Glu Pro Glu Val Lys Lys Arg Arg Leu Leu Cys Val Glu Phe	
-20 -15 -10	
GCC TCG GTC GCA AGC TGC GAT GCC GCA GTG GCT CAG TGC TTC CTG GCC	144
Ala Ser Val Ala Ser Cys Asp Ala Ala Val Ala Gln Cys Phe Leu Ala	
-5 1 5	
GAG AAC GAC TGG GAG ATG GAA AGG GCT CTG AAC TCC TAC TTC GAG CCT	192
Glu Asn Asp Trp Glu Met Glu Arg Ala Leu Asn Ser Tyr Phe Glu Pro	
10 15 20	
CCG GTG GAG GAG AGC GCC TTG GAA CGC CGA CCT GAA ACC ATC TCT GAG	240
Pro Val Glu Glu Ser Ala Leu Glu Arg Arg Pro Glu Thr Ile Ser Glu	
25 30 35 40	
CCC AAG ACC TAT GTT GAC CTA ACC AAT GAA GAA ACA ACT GAT TCC ACC	288
Pro Lys Thr Tyr Val Asp Leu Thr Asn Glu Glu Thr Thr Asp Ser Thr	
45 50 55	
ACT TCT AAA ATC AGC CCA TCT GAA GAT ACT CAG CAA GAA AAT GGC AGC	336
Thr Ser Lys Ile Ser Pro Ser Glu Asp Thr Gln Gln Glu Asn Gly Ser	
60 65 70	
ATG TTC TCT CTC ATT ACC TGG AAT ATT GAT GGA TTA GAT CTA AAC AAT	384
Met Phe Ser Leu Ile Thr Trp Asn Ile Asp Gly Leu Asp Leu Asn Asn	
75 80 85	
CTG TCA GAG AGG GCT CGA GGG GTG TGT TCC TAC TTA GCT TTG TAC AGC	432
Leu Ser Glu Arg Ala Arg Gly Val Cys Ser Tyr Leu Ala Leu Tyr Ser	
90 95 100	
CCA GAT GTG ATA TTT CTA CAG GAA GTT ATT CCC CCA TAT TAT AGC TAC	480
Pro Asp Val Ile Phe Leu Gln Glu Val Ile Pro Pro Tyr Tyr Ser Tyr	
105 110 115 120	
CTA	483
Leu	

(2) INFORMATION FOR SEQ ID NO: 191:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 444 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: DOUBLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Hypertrophic prostate
- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 182..401
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 96
region 165..384
id W56608
est
- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 45..130
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 98
region 30..115
id W56608
est
- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 127..191
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 96
region 111..175
id W56608
est
- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 401..446
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 97
region 385..430
id W56608
est
- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 311..446
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 99
region 1..136
id R17248
est
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: 13..378
 - (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5
seq RLVVSVSPQSRA/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

```

AGTGC GGCCG TC ATG GCG TCG CCC TTC AGC GGG GCG CTG CAG CTG ACG GAC    51
      Met Ala Ser Pro Phe Ser Gly Ala Leu Gln Leu Thr Asp
            -120                      -115                      -110

CTG GAT GAC TTC ATC GGG CCG TCT CAG GAG TGC ATC AAG CCT GTC AAA    99
Leu Asp Asp Phe Ile Gly Pro Ser Gln Glu Cys Ile Lys Pro Val Lys
            -105                      -100                      -95

GTG GAA AAA AGG GCG GGA AGT GGC GTG GCC AAG ATT CGC ATT GAA GAT   147
Val Glu Lys Arg Ala Gly Ser Gly Val Ala Lys Ile Arg Ile Glu Asp
            -90                      -85                      -80

GAC GGG AGC TAC TTC CAA ATT AAC CAA GAC GGC DGG ACC CGG AGG CTG   195
Asp Gly Ser Tyr Phe Gln Ile Asn Gln Asp Gly Xaa Thr Arg Arg Leu
            -75                      -70                      -65

GAG AAG GCC AAG GTC TCG CTA AAC TAC TGC NWG GCG TGC AGC GGC TGC   243
Glu Lys Ala Lys Val Ser Leu Asn Tyr Cys Xaa Ala Cys Ser Gly Cys
            -60                      -55                      -50

ATC ACC TCC GCA GAG ACC GTG CTT ATC ACC CAG CAG AGC CAC GAG GAG   291
Ile Thr Ser Ala Glu Thr Val Leu Ile Thr Gln Gln Ser His Glu Glu
            -45                      -40                      -35                      -30

CTG AAG AAG GTT CTA GAT GCT AAC AAG ATG GCG GCA CCC AGT CAG CAG   339
Leu Lys Lys Val Leu Asp Ala Asn Lys Met Ala Ala Pro Ser Gln Gln
            -25                      -20                      -15

AGG CTG GTT GTA GTT TCG GTC TCA CCA CAG TCT AGA GCA TCG CTG GCT   387
Arg Leu Val Val Val Ser Val Ser Pro Gln Ser Arg Ala Ser Leu Ala
            -10                      -5                      1

GCA CGG TTT CAG CTG AAW CCT ACA GAT ACT GCC AGG AAA TTA ACC TCA   435
Ala Arg Phe Gln Leu Xaa Pro Thr Asp Thr Ala Arg Lys Leu Thr Ser
      5                      10                      15

TTC TTT AAA
Phe Phe Lys
20

```

(2) INFORMATION FOR SEQ ID NO: 192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 44..97
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 1..54
id H30111
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 84..215
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq SLVAELLGAGSG/SH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

```
ATACTTTCTG YAGYAGTCCT GGACCTCCTG TGCAAGAACA TGAAACACCT GTGGTTCATC    60
CTCCTGCTGG TGGCAGCTCC CAG ATG GGT CCT GTC CCG ACT GCA GTT GCA GGG    113
           Met Gly Pro Val Pro Thr Ala Val Ala Gly
                           -40                -35

GCT GGC TCA CGA CTG GTA AAG CCC TCA CAG ACC CTG TCC CTC ACC TGC    161
Ala Gly Ser Arg Leu Val Lys Pro Ser Gln Thr Leu Ser Leu Thr Cys
           -30                -25                -20

GCT GTC TCT GGT GGC TCA TTA GTA GCG GAA CTT CTT CTT GGA GCT GGA    209
Ala Val Ser Gly Gly Ser Leu Val Ala Glu Leu Leu Leu Gly Ala Gly
           -15                -10                -5

TCC GGC AGT CAC CTG GGA CGG GCC TGG AGT GGA TTG GGT TCA TCT ATT    257
Ser Gly Ser His Leu Gly Arg Ala Trp Ser Gly Leu Gly Ser Ser Ile
           1                5                10

ATA GAG GCA ATA GTG GGA GTA CTT CTT ACA ATC CGT CCC TCA AGA CTC    305
Ile Glu Ala Ile Val Gly Val Leu Leu Thr Ile Arg Pro Ser Arg Leu
           15                20                25                30

GAG CCA CCA TAT CAC TGG ACA AGC CCC GCG    335
Glu Pro Pro Tyr His Trp Thr Ser Pro Ala
           35                40
```

(2) INFORMATION FOR SEQ ID NO: 193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 222..359
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 92
 region 33..170
 id T50032
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 348..393
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 160..205
 id T50032
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 189..229
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 1..41
 id T50032
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 128..196
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.4
 seq QFILLGTTSVVTA/AL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

```

GACTGATTTC GAGTTTCCGG TCAGGTTAGG CCGGGGGGGT GCGGTCCTGG TCGGAAGGAG   60
GTGGAGAGTC GGGGGTCACC AGGCCTATCC TTGGCGCCAC AGTCGGCCAC CGGGGCTCGC  120
CGCCGTC ATG GAG AGC GGA GGG CGG CCC TCG CTG TGC CAG TTC ATC CTC   169
      Met Glu Ser Gly Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu
                -20                      -15                      -10
CTG GGC ACC ACC TCT GTG GTC ACC GCC GCC CTG TAC TCC GTG TAC CGG   217
Leu Gly Thr Thr Ser Val Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg
                -5                      1                      5
CAG AAG GCC CGG GTC TCC CAA GAG CTC AAG GGA GCT AAA AAA GTT CAT   265
Gln Lys Ala Arg Val Ser Gln Glu Leu Lys Gly Ala Lys Lys Val His
                10                      15                      20
TTG GGT GAA GAT TTA AAG AGT ATT CTT TCA GAA GST CCA GGA AAA TGC   313
Leu Gly Glu Asp Leu Lys Ser Ile Leu Ser Glu Xaa Pro Gly Lys Cys
                25                      30                      35
GTG CCT TAT GCT GTT ATA GAA GGA GCT GTG CGG TCT GTT AAA GAA ACG   361
Val Pro Tyr Ala Val Ile Glu Gly Ala Val Arg Ser Val Lys Glu Thr
                40                      45                      50                      55

```

CTT AAC AGC CAG TTT GTG GAA AAC TGC AAG
Leu Asn Ser Gln Phe Val Glu Asn Cys Lys
60 65

391

(2) INFORMATION FOR SEQ ID NO: 194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 269..342
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 2..75
id R33746
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 391..459
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 124..192
id R33746
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 344..391
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 78..125
id R33746
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 397..453
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq IYIICFXLPPLFS/FN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

ATATATAAAT GTTTCATGTT ATTGGTTTTG TACCTAGTCC TTTGCATGGA TATATAGGTA 60

CCTAATGAAA ATCGAGGATC AGTGTATGAC AAATCTCCCA TCCTCCCCTT TCCTTATTGC 120

```

CTGTGTCGGC AATAGGAAGT AGAATAGTTG TGTGTTGTTT ACTTACTTGT CTGTTTTAGA 180
GAGATTTCTA TTTTGGTAG GGAATATTC TAATATGTTT TCATATCTTT ATTTCAATTT 240
GTAGTCTTTT GCATGGCTAT GTAGGGACCT AATGAAAGTC GAGTTTCATA ATATGACAGC 300
TCACDTCTTT TCCTACATAT TTCCTCACTT AGCAGTAGCT WGNKAGTTAT KTTGTGGTTA 360
TTTTATTTCA TTCTCTAGGA TCTATTCCAT TTGNNG ATG CAA GTG TGT AGA TGC 414
                               Met Gln Val Cys Arg Cys
                               -15

ATA TAT ATC ATT TGC TTC TWT CTT CCG CCA TTA TTT TCC TTT AAC 459
Ile Tyr Ile Ile Cys Phe Xaa Leu Pro Pro Leu Phe Ser Phe Asn
-10                               -5                               1

```

(2) INFORMATION FOR SEQ ID NO: 195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 44..193
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 96.1
region 1..152
id HSU78678
vrt

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 112..193
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 90..171
id N41898
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 112..193
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 95..176
id H69272
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 112..193
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 39..120
id N20619
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 44..88
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.1
seq QRLLLRFLASVIS/RK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

GGGAGGGCTA GGCTGTGCAT CCCTCCGCTC GCATTGCAGG GAG ATG GCT CAG CGA	55
Met Ala Gln Arg	
-15	
CTT CTT CTG AGG TTC CTG GCC TCT GTC ATC TCC AGG AAG CCC TCT CAR	103
Leu Leu Leu Arg Phe Leu Ala Ser Val Ile Ser Arg Lys Pro Ser Gln	
-10 -5 1 5	
GGT CAG TGG GCC ACC CCT CAC TTC CAG AGC CCT GCA GAC CCC ACA ATG	151
Gly Gln Trp Ala Thr Pro His Phe Gln Ser Pro Ala Asp Pro Thr Met	
10 15 20	
CAG TCC TGG TGG CCT GAC TGT AAC ACC CAA CCC AGC CCG GAC	193
Gln Ser Trp Trp Pro Asp Cys Asn Thr Gln Pro Ser Pro Asp	
25 30 35	

(2) INFORMATION FOR SEQ ID NO: 196:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 280 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 111..277
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 3..169
id AA149704
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 143..262
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.9
 seq FLWLITRPQPVLP/LL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

```

AAGTCCTAGG AGCTGTGGAA AGAGTAGAAG TGCCTGAATG TGGTGCTGAA TCAATACAGC   60
CAGCTGTGAG GGGAGCACTT CCTGGACCCA GGAAGGGAGA GTCTTCTTCC AAGGTCTGAA  120
TTTCCTGCTG CTGTTCACAA AG ATG CTT TTT ATC TTT AAC TTT TTG TTT TCC   172
                Met Leu Phe Ile Phe Asn Phe Leu Phe Ser
                -40                      -35

CCA CTT CCG ACC CCG GCG TTG ATC TGC ATC CTG ACA TTT GGA GCT GCC   220
Pro Leu Pro Thr Pro Ala Leu Ile Cys Ile Leu Thr Phe Gly Ala Ala
-30                -25                      -20                      -15

ATC TTC TTG TGG CTG ATC ACC AGA CCT CAA CCC GTC TTA CCT CTT CTT   268
Ile Phe Leu Trp Leu Ile Thr Arg Pro Gln Pro Val Leu Pro Leu Leu
                -10                      -5                      1

GAC CTG AAC CKG   280
Asp Leu Asn Xaa
      5
  
```

(2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 323..443
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 2..122
id R84934
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 323..390
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..68
id AA020870
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 373..443
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 92
 region 52..122
 id AA020870
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: complement(407..438)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 90
 region 42..73
 id AA187611
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 297..434
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.9
 seq SHMLQLLPSKALC/LF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

```

TTTGTGGGCT CCTCTTTGGG GTGACCACTG CTTTCAAAGC CATCTGCCAA GGCTCTCCAG   60
GGCAGGACCT GACTGGTGGG GAATGAGTGT TCAGAAGCCT TGGGAGAGGC CAAAGAGCCA  120
TTCTAGGATG RTCKGAGGAA AACCTTCCTG CAGAGGCCAG AAACCTTGAG CTTAGGTGCC   180
TGGGGACCAG CTTCGACATT CTCTCCAGTT TCTGATTCTA ATTTTGGCCA CGTGTACAAA  240
CTTTTCCAGT CTCTGAGAAG GTCCCAGVCT TTCTCAAATA TTCTGATTTT GAAAAT ATG   299
                                     Met
TAT CCA AAG TGG GAG GCC CCT GTG ACA TTT TGC CAA CTT AAA CGA GAA   347
Tyr Pro Lys Trp Glu Ala Pro Val Thr Phe Cys Gln Leu Lys Arg Glu
-45                -40                -35                -30

AAA GAC CCC CCG CAC CCG GCA CAC TCC CCC TTC CTC CAG CCC CGC TTC   395
Lys Asp Pro Pro His Pro Ala His Ser Pro Phe Leu Gln Pro Arg Phe
          -25                -20                -15

AGC CAC ATG CTC CAG CTG CTG CCC AGT AAA GCC CTG TGC CTT TTT TTC   443
Ser His Met Leu Gln Leu Leu Pro Ser Lys Ala Leu Cys Leu Phe Phe
          -10                -5                1

```

(2) INFORMATION FOR SEQ ID NO: 198:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 215 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 42..151

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98
region 1..110
id AA121585
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 143..214

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 95
region 101..172
id AA121585
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 42..136

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 1..95
id AA100539
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 143..214

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 95
region 100..171
id AA100539
est

(ix) FEATURE:

(A) NAME/KEY: sig peptide

(B) LOCATION: 36..167

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.7
seq LAERLGLFEELWA/AQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

ACTGTTTGAG GATGTAGGCA CTGGTGTGAA GGAAC ATG GCC CTG TAT CAG AGG 53
Met Ala Leu Tyr Gln Arg
-40

TGG CGG TGT CTC CGG CTC CAA GGT TTA CAG GCT TGC AGG CTA CAC ACG 101
Trp Arg Cys Leu Arg Leu Gln Gly Leu Gln Ala Cys Arg Leu His Thr
-35 -30 -25

```

GCA GTT GTG TCG ACC CCT CCA CGC TGG TTG GCA GAG CGG CTT GGC CTT      149
Ala Val Val Ser Thr Pro Pro Arg Trp Leu Ala Glu Arg Leu Gly Leu
      -20                      -15                      -10

TTT GAG GAG CTG TGG GCT GCT CAG GTA AAG AGA TTA GCA AGC ATG GCA      197
Phe Glu Glu Leu Trp Ala Ala Gln Val Lys Arg Leu Ala Ser Met Ala
      -5                      1                      5                      10

CAG AAG GAA CCC CAG ACG                                          215
Gln Lys Glu Pro Gln Thr
              15

```

(2) INFORMATION FOR SEQ ID NO: 199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 57..276
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 22..241
id C16912
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 172..260
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 64..152
id T68684
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 132..164
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 26..58
id T68684
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 98..166
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 13.8
seq XGLLLFLPLPGSLG/AE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

```

AGAGAGAGGA ACTGGGGTCT CCAGTCACGG GAGCCAGGAG CCGGCCAGGG CCGCAGSAGG      60
AAGGGAGCGA GGCTGAAGGG AACGTCGTCC TCTCAGC ATG GGG GTC CCG CGG CCT      115
                               Met Gly Val Pro Arg Pro
                               -20

CAG CCC TGG GCG STG GGG CTC CTG CTC TTT CTC CTT CCT GGG AGC CTG      163
Gln Pro Trp Ala Xaa Gly Leu Leu Leu Phe Leu Leu Pro Gly Ser Leu
      -15                      -10                      -5

GGC GCA GAA AGC CAC CTC TCC CTC CTG TAC CAC CTT ACC GCG GTG TCC      211
Gly Ala Glu Ser His Leu Ser Leu Leu Tyr His Leu Thr Ala Val Ser
      1                      5                      10                      15

TCG CCT GCC CCG GGG ACT CCT GCC TTC TGG GTG TCC GGC TGG CTG GGC      259
Ser Pro Ala Pro Gly Thr Pro Ala Phe Trp Val Ser Gly Trp Leu Gly
      20                      25                      30

CCG CAG CAG TAC CCG AGC CAK      280
Pro Gln Gln Tyr Pro Ser Xaa
      35

```

(2) INFORMATION FOR SEQ ID NO: 200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..249
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 5..252
id C18087
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 166..350
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 20..204
id AA018305
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 187..350
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 42..205
 id AA015592
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 181..350
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 33..202
 id AA018631
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 150..181
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 1..32
 id AA018631
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 158..338
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 12..192
 id R93954
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 28..162
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 13.4
 seq LVLALXLVSAALS/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

```

AAGCGCAGGC TCCCAGCCGA GTCCGTT ATG GCC GCT GCC GTC CCG AAG AGG ATG   54
                        Met Ala Ala Val Pro Lys Arg Met
                        -45                      -40

AGG GGG CCA GCA CAA GCG AAA CTG CTG CCC GGG TCG GCC ATC CAA GCC   102
Arg Gly Pro Ala Gln Ala Lys Leu Leu Pro Gly Ser Ala Ile Gln Ala
-35                      -30                      -25

CTT GTG GGG TTG GCG CGG CCG CTG GTC TTG GCG CTC VTG CTT GTG TCC   150
Leu Val Gly Leu Ala Arg Pro Leu Val Leu Ala Leu Xaa Leu Val Ser
-20                      -15                      -10                      -5

GCC GCT CTA TCC AGT GTT GTA TCA CGG ACT GAT TCA CCG AGC CCA ACC   198
Ala Ala Leu Ser Ser Val Val Ser Arg Thr Asp Ser Pro Ser Pro Thr
                        1                      5                      10

```

GTA CTC AAC TCA CAT ATT TCT ACC CCA AAT GTG AAT GCT TTA ACA CAT	246
Val Leu Asn Ser His Ile Ser Thr Pro Asn Val Asn Ala Leu Thr His	
15 20 25	
GAA AAC CAA ACC AAA CCT TCT ATT TCC CAA ATC AGC ACC ACC CTC CCT	294
Glu Asn Gln Thr Lys Pro Ser Ile Ser Gln Ile Ser Thr Thr Leu Pro	
30 35 40	
CCC AYR NCG AGT ACC AAG VNA AGT GGA GGA GCA TYT GTG GTC CCT CAT	342
Pro Xaa Xaa Ser Thr Lys Xaa Ser Gly Gly Ala Xaa Val Val Pro His	
45 50 55 60	
CCC TCG CCA GGG	354
Pro Ser Pro Gly	

(2) INFORMATION FOR SEQ ID NO: 201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 170..322
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 117..269
id HSC3DG011
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 53..184
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 1..132
id HSC3DG011
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(177..209)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 337..369
id H41589
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 137..223

(C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 13
 seq LLLVLLLVTRXRS/MP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

```

AATTTGTGCG GCGCTGGTCC CCTCAGAGGG TTCCTGCTGC TGCCGGTGCC TTGGACCCTC    60
CCCCCTCGCTT CSNGTTCTAC TGCCCCAGGA GCCCGGCGGG TCCGGGACTC CCGKCCGTGC    120
CGGTGCGGGC GCCGGC ATG TGG CTG TGG GAG GAC CAG GGC GGC CTC CTG GGC    172
          Met Trp Leu Trp Glu Asp Gln Gly Gly Leu Leu Gly
                      -25                      -20

CCT TTC TCC TTC CTG CTG CTA GTG CTG CTG CTG GTG ACG CGG ASC CGG    220
Pro Phe Ser Phe Leu Leu Leu Val Leu Leu Leu Val Thr Arg Xaa Arg
          -15                      -10                      -5

TCA ATG CCT GCC TCC TCA CCG GCA GCC TCT TCG TTC TAC TGC GCG TCT    268
Ser Met Pro Ala Ser Ser Pro Ala Ala Ser Ser Phe Tyr Cys Ala Ser
          1                      5                      10                      15

TCA GCT BTG AGC CGG TGC CCT CTT GCA GGG CCC TGC AGG TGC TCA AGC    316
Ser Ala Xaa Ser Arg Cys Pro Leu Ala Gly Pro Cys Arg Cys Ser Ser
          20                      25                      30

CCC GGG ACC GCA TTT CTG    334
Pro Gly Thr Ala Phe Leu
          35
  
```

(2) INFORMATION FOR SEQ ID NO: 202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..280
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 28..284
id R02745
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 3..176
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 6..179
id T84331
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 172..280
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 176..284
id T84331
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 27..280
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..254
id AA017512
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 27..280
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..254
id N95074
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 173..280
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 146..253
id N75564
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 65..151
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 40..126
id N75564
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 27..66
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 1..40
id N75564
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 36..119

(C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 11.6
 seq LLLLVQLLRFLRA/DG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

```

ATTCTTCCC CCCGAGCTGG GCGTGC GCGG CCGCA ATG AAC TGG GAG CTG CTG      53
                               Met Asn Trp Glu Leu Leu
                               -25

CTG TGG CTG CTG GTG CTG TGC GCG CTG CTC CTG CTC TTG GTG CAG CTG      101
Leu Trp Leu Leu Val Leu Cys Ala Leu Leu Leu Leu Leu Val Gln Leu
-20                               -15                               -10

CTG CGC TTC CTG AGG GCT GAC GGC GAC CTG ACG CTA CTA TGG GCC GAG      149
Leu Arg Phe Leu Arg Ala Asp Gly Asp Leu Thr Leu Leu Trp Ala Glu
-5                               1                               5                               10

TGG CAG GGA CGA CGC CCA GAA TGG GAG CTG ACT GAT ATG GTG GTG TGG      197
Trp Gln Gly Arg Arg Pro Glu Trp Glu Leu Thr Asp Met Val Val Trp
                               15                               20                               25

GTG ACT GGA GCC TCG AGT GGA ATT GGT GAG GAG CTG GCT TAC CAG TTG      245
Val Thr Gly Ala Ser Ser Gly Ile Gly Glu Glu Leu Ala Tyr Gln Leu
                               30                               35                               40

TCT AAA CTA GGA GTT TCT CTT GTG CTG TCA GCC AGG                        281
Ser Lys Leu Gly Val Ser Leu Val Leu Ser Ala Arg
                               45                               50
  
```

(2) INFORMATION FOR SEQ ID NO: 203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 163..344
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 35..216
id T86663
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 163..278
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 43..158
id AA055880
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 177..236
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.2
seq AFLLLVALSYTLA/RD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

```
AGAAGATAAT CACTTGGGGA AAGGAAGGTT CGTTTCTGAG TTAGCAACAA GTAAATGCAG    60
CACTAGTGGG TGGGATTGAG GTATGCCCTG GTGCATAAAT AGAGACTCAG CTGTGCTGGC   120
ACACTCAGAA GCTTGGACCG CATCCTAGCC GCCGACTCAC ACAAGGCAGA GTTGCC ATG    179
                                         Met
                                         -20

GAA AAA ATT CCA GTG TCA GCA TTC TTG CTC CTT GTG GCC CTC TCC TAC    227
Glu Lys Ile Pro Val Ser Ala Phe Leu Leu Leu Val Ala Leu Ser Tyr
          -15                      -10                      -5

ACT CTG GCC AGA GAT ACC ACA GTC AAA CCT GGA GCC AAA AAG GAC ACA    275
Thr Leu Ala Arg Asp Thr Thr Val Lys Pro Gly Ala Lys Lys Asp Thr
          1                      5                      10

AAG GAC TCT CGA CCC AAA CTG CCC CAG ACC CTC TCC AGA GGT TGG GGT    323
Lys Asp Ser Arg Pro Lys Leu Pro Gln Thr Leu Ser Arg Gly Trp Gly
          15                      20                      25

GAC CAA CTC ATC TGG ACA CGG                                344
Asp Gln Leu Ile Trp Thr Arg
          30                      35
```

(2) INFORMATION FOR SEQ ID NO: 204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 171..312
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 33..174
id T86663

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 171..288
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 41..158
id AA055880
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 127..246
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.2
seq AFLLLVALSYTLA/RD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

```

AAGATTCACA AGGCCAACAG ACAACCCAAA GTCATTAAGC CATGAGAGTG GAATGAATCT   60
ATGAAAACTC AATGAAGACA GAACAAGAGA AAAATCTTTT CAGCCACGAT GAATTAGGRG  120
AACAAG ATG TCA AAT TAC ACT GAT GCT GAG TCA AGC TTC TCA AAG CAA   168
      Met Ser Asn Tyr Thr Asp Ala Glu Ser Ser Phe Ser Lys Gln
      -40                      -35                      -30

GAG ATA ATC AGA GTT GCC ATG GAG AAA ATT CCA GTG TCA GCA TTC TTG   216
Glu Ile Ile Arg Val Ala Met Glu Lys Ile Pro Val Ser Ala Phe Leu
      -25                      -20                      -15

CTC CTT GTG GCC CTC TCC TAC ACT CTG GCC AGA GAT ACC ACA GTC AAA   264
Leu Leu Val Ala Leu Ser Tyr Thr Leu Ala Arg Asp Thr Thr Val Lys
      -10                      -5                      1                      5

CCT GGA GCC AAA AAG GAC ACA AAG GAC TCT CGA CCC AAA CCG CCC CGG   312
Pro Gly Ala Lys Lys Asp Thr Lys Asp Ser Arg Pro Lys Pro Pro Arg
      10                      15                      20

```

(2) INFORMATION FOR SEQ ID NO: 205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 96..165
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 364..433
id AA100852
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 45..95
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 314..364
id AA100852
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 14..46
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 282..314
id AA100852
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 96..202
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 65..171
id AA113841
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 31..95
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..65
id AA113841
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 290..324
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 326..360
id AA133048
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 158..191
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 2..35
id AA133048
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 169..290
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 1..122
 id AA159272
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 53..95
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 323..365
 id AA161042
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 96..138
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 365..407
 id AA161042
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 14..46
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 282..314
 id AA161042
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 3..161
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 10.6
 seq FILLIFIAEVAA/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

AC ATG CAG TTT GNA ACG TGG GCT ACT TCC TCA TCG CAG CCG GCG TTG	47
Met Gln Phe Xaa Thr Trp Ala Thr Ser Ser Ser Gln Pro Ala Leu	
-50 -45 -40	
TGG TCT TTG CTC TTG GTT TCC TGG GCT GCT ATG GTG CTA AGA CTG AGA	95
Trp Ser Leu Leu Leu Val Ser Trp Ala Ala Met Val Leu Arg Leu Arg	
-35 -30 -25	
AGC AAG TGT GCC CTC GTG ACG TTC TTC TTC ATC CTC CTC CTC ATC TTC	143
Ser Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Leu Ile Phe	
-20 -15 -10	
ATT GCT GAG GTT GCA GCT GCT GTG GTC GCC TTG GTG TAC ANC ACA ATG	191
Ile Ala Glu Val Ala Ala Ala Val Val Ala Leu Val Tyr Xaa Thr Met	
-5 1 5 10	
BCT GAG CAC TTC CTG ACG TTG CTG GTA GTG CCT GCC ATC AAG AAA GAT	239

Xaa	Glu	His	Phe	Leu	Thr	Leu	Leu	Val	Val	Pro	Ala	Ile	Lys	Lys	Asp	
				15					20					25		
TAT	GGT	TCC	CAG	GAA	GAC	TTC	ACT	CAA	GTG	TKG	AAC	ACC	ACC	ATG	AAA	287
Tyr	Gly	Ser	Gln	Glu	Asp	Phe	Thr	Gln	Val	Xaa	Asn	Thr	Thr	Met	Lys	
			30					35					40			
GGG	CTC	AAG	TGC	TGT	GGC	TTC	ACC	AAC	TAT	ACG	GAC	TGG				326
Gly	Leu	Lys	Cys	Cys	Gly	Phe	Thr	Asn	Tyr	Thr	Asp	Trp				
		45					50					55				

(2) INFORMATION FOR SEQ ID NO: 206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 140..276
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 147..283
id N36076
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..140
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 40..148
id N36076
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 287..333
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 296..342
id N36076
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..33
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 8..40
id N36076

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..333
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 9..340
id N95074
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..333
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 9..340
id AA017512
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 140..333
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 146..339
id W04626
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 5..140
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 12..147
id W04626
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 45..334
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 47..336
id H27747
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..34
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..34
id H27747
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 3..86
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.5

seq LLLLVHLLRFLRA/DG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

AA ATG AAC TGG GAG CTG CTG CTG TGG CTG CTG GTG CTG TGC GCG CTG	47
Met Asn Trp Glu Leu Leu Leu Trp Leu Leu Val Leu Cys Ala Leu	
-25 -20 -15	
CTC CTG CTC TTG GTG CAT CTG CTG CGC TTC CTG AGG GCT GAC GGC GAC	95
Leu Leu Leu Leu Val His Leu Leu Arg Phe Leu Arg Ala Asp Gly Asp	
-10 -5 1	
CTG ACG CTA CTA TGG GCC GAG TGG CAG GGA CGA CGC CCA GAA TGG GAG	143
Leu Thr Leu Leu Trp Ala Glu Trp Gln Gly Arg Arg Pro Glu Trp Glu	
5 10 15	
CTG ACT GAT ATG GTG GTG TGG GTG ACT GGA GCC TCG AGT GGA ATT GGT	191
Leu Thr Asp Met Val Val Trp Val Thr Gly Ala Ser Ser Gly Ile Gly	
20 25 30 35	
GAG GAG CTG GCT TAC CAG TTG TCT AAA CTA GGW KTT TCT CTT GTG CTG	239
Glu Glu Leu Ala Tyr Gln Leu Ser Lys Leu Gly Xaa Ser Leu Val Leu	
40 45 50	
TCA GCC AGA AGA GTG CAT GAG CTG GAA AGG GTG AAA AGA AGA TGC CTA	287
Ser Ala Arg Arg Val His Glu Leu Glu Arg Val Lys Arg Arg Cys Leu	
55 60 65	
GAG AAT GGC AAT TTA ARA GAA AAA GAT ATA CTT GTT TTG CCC CTT GGG	335
Glu Asn Gly Asn Leu Xaa Glu Lys Asp Ile Leu Val Leu Pro Leu Gly	
70 75 80	

(2) INFORMATION FOR SEQ ID NO: 207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 53..162
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 424..533
id N80896
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(283..318)

(C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 342..377
 id W16873
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 293..347
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 1..55
 id R02710
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 120..272
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 10.3
 seq VSCLTLWSPGCWP/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

```

TGC ACTATGC TTGTGTGTAT GTGTGTGCCT CTGTCTTGCT CTCTTATCTC CCAGCAGTGA    60
GAC ATTGGAC GTGTTTGCTC ATGAAGATGC AGTATATGGC TTGTCTGTGA GCCCAGTGA    119
ATG ACA ACA TTT TTG CCA GTT CCT CAG ATG ATG GCC GGG TTC TCA TTT    167
Met Thr Thr Phe Leu Pro Val Pro Gln Met Met Ala Gly Phe Ser Phe
  -50                -45                -40
GGG ACA TTC GGG AAT CCC CCC ATG GAG AGC CCT TCT GCC TGG CAA ACT    215
Gly Thr Phe Gly Asn Pro Pro Met Glu Ser Pro Ser Ala Trp Gln Thr
  -35                -30                -25                -20
ATC CAT CAG CCT TTC ATA GTG TCA TGT TTA ACC CTG TGG AGC CCA GGT    263
Ile His Gln Pro Phe Ile Val Ser Cys Leu Thr Leu Trp Ser Pro Gly
      -15                -10                -5
TGT TGG CCA CAG CCA ATT CAA AGG AAG GAG TGG GAC TCT GGG ACA TTC    311
Cys Trp Pro Gln Pro Ile Gln Arg Lys Glu Trp Asp Ser Gly Thr Phe
      1                5                10
GAA AAC CTC AGA GTT CTC TCC TGC GCT ATG GTG GAA    347
Glu Asn Leu Arg Val Leu Ser Cys Ala Met Val Glu
  15                20                25

```

(2) INFORMATION FOR SEQ ID NO: 208:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 461 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
(B) LOCATION: 168..461
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 47..340
id N39924
est

(ix) FEATURE:

- (A) NAME/KEY: other
(B) LOCATION: 169..370
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 178..379
id R61601
est

(ix) FEATURE:

- (A) NAME/KEY: other
(B) LOCATION: 359..431
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 369..441
id R61601
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 75..158
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 9.5
seq LVXFSLLATAILG/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

```

ACCATAGCAA ATTAAATGAC TGCCATAAAG TATATTTTAC TCACAGGACA GATTACAATA    60

GCCTTGATAG AATC ATG GCA TCC AAA GGG ATG CGC CAT TTT TGC TTG ATT    110
      Met Ala Ser Lys Gly Met Arg His Phe Cys Leu Ile
                        -25                      -20

TCA GAG CAG TTG GTG TYC TTT AGT CTT CTT GCA ACA GCG ATT TTG GGA    158
Ser Glu Gln Leu Val Xaa Phe Ser Leu Leu Ala Thr Ala Ile Leu Gly
-15                      -10                      -5

GCA GTT TCC TGG CAG CCA ACA AAT GGA ATT TTC TTG AGC ATG TTT CTA    206
Ala Val Ser Trp Gln Pro Thr Asn Gly Ile Phe Leu Ser Met Phe Leu
  1                      5                      10                      15

ATC GTT TTG CCA TTG GAA TCC ATG GCT CAT GGG CTC TTC CAT GAA TTG    254
Ile Val Leu Pro Leu Glu Ser Met Ala His Gly Leu Phe His Glu Leu
      20                      25                      30

GGT AAC TGT TTA GGA GGA ACA TCT GTT GGA TAT GCT ATT GTG ATT CCC    302
Gly Asn Cys Leu Gly Gly Thr Ser Val Gly Tyr Ala Ile Val Ile Pro

```

35	40	45	
ACC AAC TTC TGC AGT CCT GAT GGT CAG CCA ACA CTG CTT CCC CCA GAA			350
Thr Asn Phe Cys Ser Pro Asp Gly Gln Pro Thr Leu Leu Pro Pro Glu			
50	55	60	
CAT GTA CAG GAG TTA AAT TTG AGG TCT ACT GGC ATG CTC AAT GCT ATC			398
His Val Gln Glu Leu Asn Leu Arg Ser Thr Gly Met Leu Asn Ala Ile			
65	70	75	80
CAA AGA TTT TTT GCA TAT CAT ATG ATT GAG ACC TAT GGA TGT GAC TAT			446
Gln Arg Phe Phe Ala Tyr His Met Ile Glu Thr Tyr Gly Cys Asp Tyr			
85	90	95	
TCC ACA AGT GGA CTG			461
Ser Thr Ser Gly Leu			
100			

(2) INFORMATION FOR SEQ ID NO: 209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(31..239)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 3..211
id N27605
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..111)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..110
id N78549
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 78..140
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.3
seq VLPVILLLLGAHP/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:


```

AAGAGCAGAG CCGGAAGAAG GCGGGACGAA CCGGAAGAGG GTGAAATGCT TTCGGTAGGC      60
ACTCCACGGC TGTGAAG ATG GCG GCG GCT GCG TGG CTT CAG GTG TTG CCT      110
          Met Ala Ala Ala Ala Trp Leu Gln Val Leu Pro
          -20                      -15

GTC ATT CTT CTG CTT CTG GGA GCT CAC CCG TCA CCA CTG TCG TTT TTC      158
Val Ile Leu Leu Leu Leu Gly Ala His Pro Ser Pro Leu Ser Phe Phe
-10                      -5                      1                      5

AGT GCG GGA CCG GCA ACC GTA GCT GCT GCC GAC CGG TCC AAA TGG CAC      206
Ser Ala Gly Pro Ala Thr Val Ala Ala Ala Asp Arg Ser Lys Trp His
          10                      15                      20

RKT CCG ATA CCG TCG GGG AAA AAT TAT TTT AGT TTT GGA AAG ATC CTC      254
Xaa Pro Ile Pro Ser Gly Lys Asn Tyr Phe Ser Phe Gly Lys Ile Leu
          25                      30                      35

TTC AGA AAT ACC ACT ATC TTC CTG AAG TTT GAT GGA GAA CGA      296
Phe Arg Asn Thr Thr Ile Phe Leu Lys Phe Asp Gly Glu Arg
          40                      45                      50

```

(2) INFORMATION FOR SEQ ID NO: 210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 118..281
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 78..241
id R57572
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 38..91
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..54
id R57572
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 90..122
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93
region 52..84
id R57572
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 117..272
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 59..214
id W55468
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 273..328
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 214..269
id W55468
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 130..456
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 9.1
seq LVLAVLFFHQLVG/DP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

ACTTTGTCAT	TCAGCTGCCT	GCTGCCTCCG	CAGCGTCCCC	CCAGCTCTCC	CTGTGCTAAC	60
TGCCTGCACC	TTGGACAGAG	CGGGTGC	GCA AATCAGAAGG	ATTAGTTGGG	ACCTGCCCTT	120
GGCGACCCC	ATG GCA TCC CCC AGA ACC GTA ACT ATT GTG GCC CTC TCA GTG	171				
	Met Ala Ser Pro Arg Thr Val Thr Ile Val Ala Leu Ser Val					
	-105	-100				
GCC CTG GGA CTC TTC TTT GTT TTC ATG GGG ACT ATC AAG CTG ACC CCC	219					
Ala Leu Gly Leu Phe Phe Val Phe Met Gly Thr Ile Lys Leu Thr Pro						
-95	-90	-85	-80			
AGG CTC AGC AAG GAT GCC TAC AGT GAG ATG AAA CGT GCN NAC AAG AGC	267					
Arg Leu Ser Lys Asp Ala Tyr Ser Glu Met Lys Arg Ala Xaa Lys Ser						
-75	-70	-65				
TAT GTT CGA GCC CTC CCT CTG CTG AAG AAA ATG GGG ATC AAT TCC ATT	315					
Tyr Val Arg Ala Leu Pro Leu Leu Lys Lys Met Gly Ile Asn Ser Ile						
-60	-55	-50				
CTC CTC CGA AAA AGC ATT GGT GCC CTT GAA GTG GCC TGT GGC ATC GTC	363					
Leu Leu Arg Lys Ser Ile Gly Ala Leu Glu Val Ala Cys Gly Ile Val						
-45	-40	-35				
ATG ACC CTT GTG CCT GGG CGT CCC AAA GAT GTG GCC AAC TTC TTC CTA	411					
Met Thr Leu Val Pro Gly Arg Pro Lys Asp Val Ala Asn Phe Phe Leu						
-30	-25	-20				

CTG TTG CTG GTG TTG GCT GTG CTC TTC TTC CAC CAG CTG GTC GGT GAT 459
Leu Leu Leu Val Leu Ala Val Leu Phe Phe His Gln Leu Val Gly Asp
-15 -10 -5 1

CCT CTC AAA 468
Pro Leu Lys

(2) INFORMATION FOR SEQ ID NO: 211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 88..221
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 84..217
id AA021055
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 5..74
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..70
id AA021055
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 88..221
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 84..217
id W98068
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 5..74
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..70
id W98068
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 88..191
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 11..114
id AA059040
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 91..204
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.8
seq LLLLCALHSHIYC/IK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

```
CATAAAATTT GAGGATATCA GCTGATTATT TTTTCTCCM ASAATGAAAA TCAAGCAGAA    60
TTGATTCCTA CACGAAAAAA AAGCACACGA ATG CCA AAC CTT TCC TTT GGT GGA    114
                               Met Pro Asn Leu Ser Phe Gly Gly
                               -35

CTG GAC ACT AAC CAG ATG AGA GTA AAT TTC TTA TCC GTG GAC GTA TGT    162
Leu Asp Thr Asn Gln Met Arg Val Asn Phe Leu Ser Val Asp Val Cys
-30                -25                -20                -15

AAG CTA CTG CTG CTG TGT GCT CTC CAC AGC CAT ATT TAT TGT ATT AAA    210
Lys Leu Leu Leu Leu Cys Ala Leu His Ser His Ile Tyr Cys Ile Lys
                -10                -5                1

CAA TCA GCA CTT CGG                                225
Gln Ser Ala Leu Arg
                    5
```

(2) INFORMATION FOR SEQ ID NO: 212:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 470 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 134..378
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 115..359
id R67703
est

(ix) FEATURE:

- (A) NAME/KEY: other
 - (B) LOCATION: 23..135
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 92
region 5..117
id R67703
est
- (ix) FEATURE:
- (A) NAME/KEY: other
 - (B) LOCATION: 134..318
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 98
region 115..299
id H42383
est
- (ix) FEATURE:
- (A) NAME/KEY: other
 - (B) LOCATION: 20..135
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 98
region 2..117
id H42383
est
- (ix) FEATURE:
- (A) NAME/KEY: other
 - (B) LOCATION: 193..383
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 100
region 87..277
id W90193
est
- (ix) FEATURE:
- (A) NAME/KEY: other
 - (B) LOCATION: 134..192
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 96
region 29..87
id W90193
est
- (ix) FEATURE:
- (A) NAME/KEY: other
 - (B) LOCATION: 417..454
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 92
region 314..351
id W90193
est
- (ix) FEATURE:
- (A) NAME/KEY: other
 - (B) LOCATION: 288..470
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 97
region 1..183
id R53752
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 258..422
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.8
seq XXLLLLNVGQLLA/QT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

```

AACCACGGT GGGGGGAGCG CGGCCATGGC GCTCCTGCTT TCGGTGCTGC GTGTACTGCT    60
GGGCGGCTTC TTCGCGCTCG TGGGGTTGGC CAAGCTCTCG GAGGAGATCT CGGCTCCAGT    120
TTCGGAGCGG RTGRAATGCC CTGTTCTGTC AGTTTGCTGA TGTGTTCCCG CTGAAGGTAT    180
TTGGCTACCA GCCAGATCCC CTGAACTACC AAATAGCTGT GGGCTTCTG GAACTGCTGG    240
CTGGGTTGCT GCTGGTC ATG GGC CCA CCG ATG CTG CAA GAG ATC AGT AAC    290
          Met Gly Pro Pro Met Leu Gln Glu Ile Ser Asn
          -55                -50                -45

TTG TTC TTG ATT CTG CTC ATG ATG GGG GCT ATC TTC ACC TTG GCA GCT    338
Leu Phe Leu Ile Leu Leu Met Met Gly Ala Ile Phe Thr Leu Ala Ala
          -40                -35                -30

CTG AAA GAG TCA CTA AGC ACC TGT ATC CCA GCC ATT GTC TGC CTG NGG    386
Leu Lys Glu Ser Leu Ser Thr Cys Ile Pro Ala Ile Val Cys Leu Xaa
          -25                -20                -15

TDN CTG CTG CTG CTG AAT GTC GGC CAG CTC TTA GCC CAG ACT AAG AAG    434
Xaa Leu Leu Leu Leu Asn Val Gly Gln Leu Leu Ala Gln Thr Lys Lys
          -10                -5                1

GTG GTC AGA CCC ACT AGG AAG AAG ACT CTA AGT ACA    470
Val Val Arg Pro Thr Arg Lys Lys Thr Leu Ser Thr
    5                10                15

```

(2) INFORMATION FOR SEQ ID NO: 213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 4..55
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 19..70

id T18977
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 141..195
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 157..211
id T18977
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 92..137
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 109..154
id T18977
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 245..355
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 1..111
id HSC12A111
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 321..355
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 1..35
id W73324
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 133..345
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.6
seq VVXFLLLLLAXLIA/TY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

```
AAGCAGCTTC CAGGATCCTG AGATCCGGAG CAGCCGGGGT CGGAGCGGCT CCTCAAGAGT   60
TACTGATCTA TNNATGGCAG AGAAAAAAAA ATTGTGACCA GAGACGTGTA GCAATGAACA  120
AGGAACRTCA TA ATG RWN NNK TTC ACA GAC CCC TCT TCA GTG AAT GAA AAG   171
      Met Xaa Xaa Phe Thr Asp Pro Ser Ser Val Asn Glu Lys
        -70                -65                -60

AAG AGG AGG GAG CGG GAA GAA AGG CAG AAT ATT GTC CTG TGG AGA CAG   219
Lys Arg Arg Glu Arg Glu Glu Arg Gln Asn Ile Val Leu Trp Arg Gln
      -55                -50                -45
```

ACCTTTCTGG	GTTGAGCATG	GCTGAAGTGA	CTCAGCCCAT	GGGAGGTTTC	CTAGGAGNAA	60
CAGGCTCCAC	TTGCTGCCTC	TCTGCGTGAA	CTCCGTGTGC	CGGCAACCTG	GCGACCAGAC	120
TCCTGCCTTC	GGAGGGGCTG	GGGCTCCAGG	ACCTGAGTGC	CCCCCRNKGT	TGGAAGGCGG	180
TGTCATATGT	GCACAGAAGC	CAAAAAGCAT	TGCTGGTATT	TCGAAGGACT	CTATCCAACC	240
YHTTATAT	ATG CCG CTC CTA CGA GGA	CTG CTG TGG	STC CAG GTG CTG TGT			290
	Met Pro Leu Leu Arg Gly	Leu Leu Trp	Xaa Gln Val Leu Cys			
	-15	-10	-5			
GCG GGC CCT CTC CAT ACA GAG						311
Ala Gly Pro Leu His Thr Glu						

1

5

(2) INFORMATION FOR SEQ ID NO: 215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 121..355
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 31..265
id T78247
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 121..355
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 6..240
id W17118
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 121..355
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 11..245
id N88433
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 121..336
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 32..247
id R35014
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 121..329
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 9..217
id AA074562

est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 159..218
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.4
seq AVVGCLLVPPAEA/NK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

```

AAGAGGCGGA GATGGCGGAG GCGGGTGGGA CGTGATGCGC GGGTCAGAGC CGGGCCTTGA   60
GAAGGAACTG GAGGCCCCCTG GCAGCGGTGT CCCCTCGAGG ACCCCTCTGC CGGGCTCACC  120
AGGTGTCCGG CTTTGCTGGC CCAGCAAGCC TGATAAGC ATG AAG CTC TTA TCT TTG   176
                               Met Lys Leu Leu Ser Leu
                               -20                               -15

GTG GCT GTG GTC GGG TGT TTG CTG GTG CCC CCA GCT GAA GCC AAC AAG   224
Val Ala Val Val Gly Cys Leu Leu Val Pro Pro Ala Glu Ala Asn Lys
                               -10                               -5                               1

AGT TCT GAA GAT ATC CRG TGC AAA TGC ATC TGT CCA CCT TAT AGA AAC   272
Ser Ser Glu Asp Ile Xaa Cys Lys Cys Ile Cys Pro Pro Tyr Arg Asn
                               5                               10                               15

ATC AGT GGG CAC ATT TAC AAC CAG AAT GTA TCC CAG AAG GAC TGC AAC   320
Ile Ser Gly His Ile Tyr Asn Gln Asn Val Ser Gln Lys Asp Cys Asn
                               20                               25                               30

TGC CTG CAC GTG GTG GAG CCC ATG CCA GTG CCG   353
Cys Leu His Val Val Glu Pro Met Pro Val Pro
                               35                               40                               45

```

(2) INFORMATION FOR SEQ ID NO: 216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 15..332
id HUM085F04B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 139..249
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 187..297
id H85714
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 249..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 298..368
id H85714
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 86..148
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 133..195
id H85714
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 135..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 80..264
id R77008
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 86..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 94..327
id H49758
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 135..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 53..237
id AA056366
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 114..185
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9
seq LLLPRVLLTMASG/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

```

AATTGGCTGG CTCTGGAGGC GCAGGTGGTC CTTCTTCTAC TGTCACATGG TGC GCGCTGT      60
TTTCTAATCA CGKGGCTGCC ACCCAGGCCT CTCTGCTCCT GTCKTKTGTT TGG ATG      116
                                   Met
CCG GCG CTG CTG CCT GTG GCC TCC CGC CTT TTG TTG CTA CCC CGA GTC      164
Pro Ala Leu Leu Pro Val Ala Ser Arg Leu Leu Leu Leu Pro Arg Val
               -20                      -15                      -10
TTG CTG ACC ATG GCC TCT GGA AGC CCT CCG ACC CAG CCC TCG CCG GCC      212
Leu Leu Thr Met Ala Ser Gly Ser Pro Pro Thr Gln Pro Ser Pro Ala
               -5                      1                      5
TCG GAT TCC GGC TCT GGC TAC GTT CCG GGC TCG GTC TCT GCA GCC TTT      260
Ser Asp Ser Gly Ser Gly Tyr Val Pro Gly Ser Val Ser Ala Ala Phe
   10                      15                      20                      25
GTT ACT TGC CCC AAC GAG AAG GTC GCC AAG GAG ATC GCC AGG GCC GTC      308
Val Thr Cys Pro Asn Glu Lys Val Ala Lys Glu Ile Ala Arg Ala Val
               30                      35                      40
GGG GAG AAG CGG      320
Gly Glu Lys Arg
               45

```

(2) INFORMATION FOR SEQ ID NO: 217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 121..381
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 73..333
id H95186
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 72..133
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 25..86
id H95186
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
 (B) LOCATION: 28..351
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.9
 seq LLGLLSAEQLAEA/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

```

ACGGGTGCCG GGTGGAGCGA ASACGGA ATG TGT CTC CTG CTG GGG GCC ACG GGC      54
                        Met Cys Leu Leu Leu Gly Ala Thr Gly
                        -105                        -100

GTC GGG AAG ACG CTG CTG GTG AAA CGG CTG CAG GAG GTG AGC TCC CGG      102
Val Gly Lys Thr Leu Leu Val Lys Arg Leu Gln Glu Val Ser Ser Arg
                        -95                        -90                        -85

GAT GGG AAA GGC GAC CTG GGG GAG CCG CCC CCG ACA CGG CCC ACG GTG      150
Asp Gly Lys Gly Asp Leu Gly Glu Pro Pro Pro Thr Arg Pro Thr Val
                        -80                        -75                        -70

GGC ACC AAT CTT ACT GAC ATC GTG GCA CAG AGA AAG ATC ACC ATC CGG      198
Gly Thr Asn Leu Thr Asp Ile Val Ala Gln Arg Lys Ile Thr Ile Arg
                        -65                        -60                        -55

GAG CTT GGG GGG TGC ATG GGC CCC ATC TGG TCC AGT TAC TAT GGA AAC      246
Glu Leu Gly Gly Cys Met Gly Pro Ile Trp Ser Ser Tyr Tyr Gly Asn
                        -50                        -45                        -40

TGC CGT TCT CTC CTG TTT GTG ATG GAC GCC TCT GAC CCC ACC CAG CTC      294
Cys Arg Ser Leu Leu Phe Val Met Asp Ala Ser Asp Pro Thr Gln Leu
                        -35                        -30                        -25                        -20

TCT GCA TTM SGT GTG CAG CTC TTA GGT CTC CTT TCT GCA GAA CAA CTT      342
Ser Ala Xaa Xaa Val Gln Leu Leu Gly Leu Leu Ser Ala Glu Gln Leu
                        -15                        -10                        -5

GCA GAA GCA TCG GTG CTG ATA CTC TTC AAT AAA ATC GAC AAC      384
Ala Glu Ala Ser Val Leu Ile Leu Phe Asn Lys Ile Asp Asn
      -           1           5           10

```

(2) INFORMATION FOR SEQ ID NO: 218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 94..197
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 92..195
id T93931
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 2..45
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..44
id T93931
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 53..97
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 52..96
id T93931
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 190..234
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 187..231
id T93931
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 138..196
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 241..299
id N25481
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 190..234
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 292..336
id N25481
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 94..211
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 65..182
id W19370
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 94..196
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 56..158
id N35539
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 190..234
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 151..195
id N35539
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 56..97
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 19..60
id N35539
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 94..193
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 96..195
id W87436
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 2..49
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 7..54
id W87436
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 75..197
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.7
seq LLCLGQLHHPGLG/RV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

```
AAAGTTTGTT CCCCAGATTC GGAGCCTAGG AGCCCCCGCG GGCTGCGGCG CAGGTGCCCT    60
CGGCCTTAGT CGGG ATG GAG CTG CCT GCK GTG AAC CTT GAA AGT GAT TCT    110
      Met Glu Leu Pro Ala Val Asn Leu Glu Ser Asp Ser
      -40                      -35                      -30
```

CCT AGG TCA CTG GCT GCT GAC AAC CTG GGG CTG CAT TGT ATT CTC AGG	158
Pro Arg Ser Leu Ala Ala Asp Asn Leu Gly Leu His Cys Ile Leu Arg	
-25 -20 -15	
CTC CTA TGC CTG GGC CAA CTT CAC CAT CCT GGC CTT GGG CGT GTG GGC	206
Leu Leu Cys Leu Gly Gln Leu His His Pro Gly Leu Gly Arg Val Gly	
-10 -5 1	
TGT GGC TCA GCG GGA CTC CAT CGA CGC CGG	236
Cys Gly Ser Ala Gly Leu His Arg Arg	
5 10	

(2) INFORMATION FOR SEQ ID NO: 219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 145..240
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 99..194
id N28787
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 45..139
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..95
id N28787
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 253..326
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 207..280
id N28787
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 145..239
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 114..208

id AA102327
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 59..139
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 30..110
id AA102327
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 31..63
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..33
id AA102327
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 277..311
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 250..284
id AA102327
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 145..240
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 101..196
id AA019783
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 253..326
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 209..282
id AA019783
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 79..139
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 37..97
id AA019783
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 145..240
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 95
region 115..210
id AA059290
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 41..139
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 13..111
id AA059290
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 253..319
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 223..289
id AA059290
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 145..240
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 102..197
id H86516
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 253..326
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 210..283
id H86516
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 75..139
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 34..98
id H86516
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 171..323
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.6
seq PALILLFALGSLG/SG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

```

GGTGCTGTTG CCATCATGGC TGACCCCGAC CCCCAGTACC CTCGCTCCTC GATCGAGGAC 120
GACTTCAACT ATGGCAGCAA GCGTKGGCYT CSGCCACCGT GCACATCCGA ATG GCC 176
                                         Met Ala
                                         -50

TTT CTG AGA AAA GTC TAC AGC ATT CTT TCT CTG CAG GTT CTC TTA ACT 224
Phe Leu Arg Lys Val Tyr Ser Ile Leu Ser Leu Gln Val Leu Leu Thr
          -45                      -40                      -35

ACA GTG ACT TCA ACA GTT TTT TTA TAC TTT GAG TCT GTA CGG ACA TTT 272
Thr Val Thr Ser Thr Val Phe Leu Tyr Phe Glu Ser Val Arg Thr Phe
          -30                      -25                      -20

GTA CAT GAG AGT CCT GCC TTA ATT TTG CTG TTT GCC CTC GGA TCT CTG 320
Val His Glu Ser Pro Ala Leu Ile Leu Leu Phe Ala Leu Gly Ser Leu
          -15                      -10                      -5

GGT TCG GGG 329
Gly Ser Gly
1

```

(2) INFORMATION FOR SEQ ID NO: 220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 23..202
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..180
id W88492
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 25..111
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6
seq PTLAIALAANAWA/FV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

```

ACCATATGGG TGGTGTGGAT CGTC ATG TAT ACT TAC GGC AAC AAG CAG CAC 51
Met Tyr Thr Tyr Gly Asn Lys Gln His
          -25

```

```

AAC AGT CCC ACC TGG GAT GAC CCC ACG CTG GCC ATC GCC CTC GCC GCC      99
Asn Ser Pro Thr Trp Asp Asp Pro Thr Leu Ala Ile Ala Leu Ala Ala
-20                      -15                      -10                      -5

AAT GCC TGG GCC TTC GTC CTC TTC TAC GTC ATC CCC GAG GTC TCC CAG      147
Asn Ala Trp Ala Phe Val Leu Phe Tyr Val Ile Pro Glu Val Ser Gln
                      1                      5                      10

GTG ACC AAG TCC AGC CCA GAG CAA AGC TAC CAG GGG GAC ATG TAC CCC      195
Val Thr Lys Ser Ser Pro Glu Gln Ser Tyr Gln Gly Asp Met Tyr Pro
                      15                      20                      25

ACC CGG GAC TTG                                                    207
Thr Arg Asp Leu
                      30

```

(2) INFORMATION FOR SEQ ID NO: 221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(136..167)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 239..270
id H62766
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 70..165
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6
seq WILVLALPLTVWP/WL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

```

ACTTTCAGTT TCCTTCTTCC AGCACGGAGT ACACTGCTCT GCCTCCACTT AGATTACTTC      60

AGAAATGAA ATG CAG CAA ATA TTT ATC CAG CAG TGC AGG GAG TTG AAC TTT      111
Met Gln Gln Ile Phe Ile Gln Gln Cys Arg Glu Leu Asn Phe
                      -30                      -25                      -20

TGG AGT CGG GAA CCT TGG ATT CTT GTT CTG GCT CTG CCA CTT ACT GTG      159
Trp Ser Arg Glu Pro Trp Ile Leu Val Leu Ala Leu Pro Leu Thr Val
                      -15                      -10                      -5

```

195

CGC ATC CGC GCA GTT GGC CTC CTG ACC GTC ATC AGC AAA GGC TGC AGC 310
Arg Ile Arg Ala Val Gly Leu Leu Thr Val Ile Ser Lys Gly Cys Ser
40 45 50

TTG AAC TGC GTG GAT SAC TCA CAG GAC TAC TAC GTG GGC AAG AAG AAC 358
 Leu Asn Cys Val Asp Xaa Ser Gln Asp Tyr Tyr Val Gly Lys Lys Asn
 55 60 65

ATC ACG TGC TGT GAC 373
 Ile Thr Cys Cys Asp
 70

(2) INFORMATION FOR SEQ ID NO: 223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..247
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
 region 1..247
 id AA166578
 est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 4..51
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.1
 seq QACLLGLFALILS/GK

-(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

AGA ATG GGA CTC CAA GCC TGC CTC CTA GGG CTC TTT GCC CTC ATC CTC 48
 Met Gly Leu Gln Ala Cys Leu Leu Gly Leu Phe Ala Leu Ile Leu
 -15 -10 -5

TCT GGC AAA TGC AGT TAC AGC CCG GAG CCC GAC CAG CGG AGG ACG CTG 96
 Ser Gly Lys Cys Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr Leu
 1 5 10 15

CCC CCA GGC TGG GTG TCC CTG GGC CGT GCG GAC CCT GAG GAA GAG CTG 144
 Pro Pro Gly Trp Val Ser Leu Gly Arg Ala Asp Pro Glu Glu Glu Leu
 20 25 30

AGT CTC ACC TTT GCC CTG AGA CAG CAG AAT GTG GAA AGA CTC TCG GAG 192
 Ser Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg Leu Ser Glu
 35 40 45

CTG GTG CAG GCT GTG TCG GAT CCC AGC TCT CCT CAA TAC GGA AAA TAC 240

Leu Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln Tyr Gly Lys Tyr
50 55 60

CTG ACC CGT
Leu Thr Arg
65

249

(2) INFORMATION FOR SEQ ID NO: 224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(141..361)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 146..366
id H19708
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 143..264
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 143..264
id H20045
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..74
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 4..77
id H20045
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 143..382
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 8..247
id C15772
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 157..341
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 1..185
 id H67240
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 340..382
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 185..227
 id H67240
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 172..382
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 1..211
 id HUM408E11B
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 2..88
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7
 seq LGSGLGLSPGTSS/GR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

G ATG AGG CCG GGG CAG GTC TCC CTC CTG GGT CCT GAT GCT GTT TCT GTG	49
Met Arg Pro Gly Gln Val Ser Leu Leu Gly Pro Asp Ala Val Ser Val	
-25 -20 -15	
CTC GGC TCT GGC TTG GGC CTC AGC CCT GGC ACC AGC TCT GGC CGC AAC	97
Leu Gly Ser Gly Leu Gly Leu Ser Pro Gly Thr Ser Ser Gly Arg Asn	
-10 -5 1	
CCT GAC CCT GGC TCT GGG CCG GGC ACT CTG CCG GRT YCC AGC DTC CAA	145
Pro Asp Pro Gly Ser Gly Pro Gly Thr Leu Pro Xaa Xaa Ser Xaa Gln	
5 10 15	
AAC CCC TCC CCG GCT CCA GAT CCA CCC CCA GCC CTA CTC CTG TGG AAT	193
Asn Pro Ser Pro Ala Pro Asp Pro Pro Pro Ala Leu Leu Leu Trp Asn	
20 25 30 35	
CTT CTG ACC CAA AGG CTG GGC ACG ACG CTG GTC CCG ACC TTG TGC CCA	241
Leu Leu Thr Gln Arg Leu Gly Thr Thr Leu Val Pro Thr Leu Cys Pro	
40 45 50	
GCC CAG ACC TTG ATC CTG TGC CCA GCC CAG ACC CTG ATC CTG TGC CCA	289
Ala Gln Thr Leu Ile Leu Cys Pro Ala Gln Thr Leu Ile Leu Cys Pro	
55 60 65	
RCC CTG ATC CCA ACC CTG TGT CCT GCC CTG AMC CCT GTT CTC CCA STC	337
Xaa Leu Ile Pro Thr Leu Cys Pro Ala Leu Xaa Pro Val Leu Pro Xaa	

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 138..186
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 14..62
id AA111755
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 83..286
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.7
seq IACLAWWIGGGSG/XN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

```

AAAGACTTTG CGAASGCTGC GCTCGCGCCC GGATCCCTCA GGCGGCTGCA GGCTTCAGCC      60
TGC GCTGGTT GGTGAAACAG AG ATG TCA GAA AAG GAG AVC AAC TTC CCG CCA      112
      Met Ser Glu Lys Glu Xaa Asn Phe Pro Pro
                        -65                      -60

CTG CCC AAG TTC ATC CCT GTG AAG CCC TGC TTC TAC CAG AAC TTC TCC      160
Leu Pro Lys Phe Ile Pro Val Lys Pro Cys Phe Tyr Gln Asn Phe Ser
      -55                      -50                      -45

GAC GAG ATC CCA GTG GAG CAC CAG GTC CTG GTG AAG AGG ATC TAC CGG      208
Asp Glu Ile Pro Val Glu His Gln Val Leu Val Lys Arg Ile Tyr Arg
      -40                      -35                      -30

CTG TGG ATG TTT TAC TGC GCC ACC CTC GGC GTC AAC CTC ATT GCC TGC      256
Leu Trp Met Phe Tyr Cys Ala Thr Leu Gly Val Asn Leu Ile Ala Cys
      -25                      -20                      -15

CTG GCC TGG TGG ATC GGC GGA GGC TCG GGG NNB AAC TTC GGC CTG GCC      304
Leu Ala Trp Trp Ile Gly Gly Gly Ser Gly Xaa Asn Phe Gly Leu Ala
      -10                      -5                      1                      5

TTC GTG TGG CTG CTC CTG TTC ACG CCT TGC GGC TAC GTG TGC TGG TTC      352
Phe Val Trp Leu Leu Leu Phe Thr Pro Cys Gly Tyr Val Cys Trp Phe
      10                      15                      20

CGG CCT GTC TAC AAG GCC TTC CGA GCC GAC AGC TCC TTT AAT TTC ATG      400
Arg Pro Val Tyr Lys Ala Phe Arg Ala Asp Ser Ser Phe Asn Phe Met
      25                      30                      35

GGC CTG      406
Ala Leu
      40

```

(2) INFORMATION FOR SEQ ID NO: 227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(68..131)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 392..455
id W22335
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 288..347
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 9..68
id H70453
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 159..227
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7
seq ILRLYFFFLQLAHS/GY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

```

ACGAAATGGT ATTGACATCT TGGTTGGAAC ACCTGGTCGT ATCAAAGACC ATCTGCAGAG   60
TGGCCGATTG GATCTTTCTA AACTGCGACA TGTGTGCTT GATGAAGTGG ATCAGATGTT   120
AGATTTAGGT TTCGCTGAAC AAGTTGAAGA TATTATTC ATG AAT CCT ACA AAA CTG   176
                               Met Asn Pro Thr Lys Leu
                               -20

ATT CTG AAG ACA ATC CTC AGA CTT TAC TTT TTT CTG CAA CTT GCC CAC   224
Ile Leu Lys Thr Ile Leu Arg Leu Tyr Phe Phe Leu Gln Leu Ala His
      -15                      -10                      -5

AGT GGG TAT ACA AAG TTG CAA AAA AAA TAC ATG AAA TCC AGA TAT GAA   272
Ser Gly Tyr Thr Lys Leu Gln Lys Lys Tyr Met Lys Ser Arg Tyr Glu
      1                      5                      10                      15

CAG GTT GAC CTT GTT GGR AAA ATG WCT CAA AAG GCT GCA ACT ACT GTG   320

```

Gln Val Asp Leu Val Gly Lys Met Xaa Gln Lys Ala Ala Thr Thr Val
20 25 30

GRA CAT TTG GCC ATC CAG TGT CAT TGG
Xaa His Leu Ala Ile Gln Cys His Trp
35 40

347

(2) INFORMATION FOR SEQ ID NO: 228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 12..70
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..59
id AA013305
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 197..250
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 189..242
id AA013305
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 250..297
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 243..290
id AA013305
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 136..199
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 236..299
id R48472
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 37..101
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 135..199
 id R48472
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 38..106
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.7
 seq SXXCFVSVPPASA/IP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

```

AACCCGGGAC CGAGCTGGGG TCTTGAGGA AGAGAGG ATG GCG TCG TCG AGC CCT      55
                               Met Ala Ser Ser Ser Pro
                               -20

GAC TCC CCA TGT TCC TGS NAC TGC TTT GTC TCC GTG CCC CCG GCC TCA      103
Asp Ser Pro Cys Ser Xaa Xaa Cys Phe Val Ser Val Pro Pro Ala Ser
   -15                -10                -5

GCC ATC CCG GST GTG AKC TTK GCC NNH AAC TCG GAC SGA CCC CGG GAC      151
Ala Ile Pro Xaa Val Xaa Xaa Ala Xaa Asn Ser Asp Xaa Pro Arg Asp
   1                5                10                15

GAG GTG CAG GAG GTG GTG TTT GTC CCC GCA GGC ACT CAC ACT CCT GGG      199
Glu Val Gln Glu Val Val Phe Val Pro Ala Gly Thr His Thr Pro Gly
                20                25                30

AGC CGG CTC CAG TGC ACC TAC ATT GAA GTG GAA CAG GTG TCG AAG ACG      247
Ser Arg Leu Gln Cys Thr Tyr Ile Glu Val Glu Gln Val Ser Lys Thr
                35                40                45

CAC GCT GTG ATT CTG AGC CGT CCT TCT TGG CTA TGG GGG GCT GAG ATG      295
His Ala Val Ile Leu Ser Arg Pro Ser Trp Leu Trp Gly Ala Glu Met
                50                55                60

GGC GMV ACG AGC ATG GTG TCT GCA TTG GCA ACG AGG CTG TGT GGA CGA      343
Gly Xaa Thr Ser Met Val Ser Ala Leu Ala Thr Arg Leu Cys Gly Arg
   65                70                75

AGG AGC CAG TTG GGG AGG GCN GKN GCC CTS CTG GGC ATG GAC CTA CTC      391
Arg Ser Gln Leu Gly Arg Ala Xaa Ala Leu Leu Gly Met Asp Leu Leu
   80                85                90                95

AGG TGC AGA CCC TGC                                          406
Arg Cys Arg Pro Cys
                100
  
```

(2) INFORMATION FOR SEQ ID NO: 229:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 308 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE

- (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 128..197
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 158..227
id AA249540
est
- (ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 241..309
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 267..335
id AA249540
est
- (ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 164..240
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 58..134
id N46699
est
- (ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 128..161
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 23..56
id N46699
est
- (ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: complement(224..309)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 104..189
id W39777
est
- (ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 233..309
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 13..89
id AA036848
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 233..309
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 13..89
id AA133513
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 171..287
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7
seq XLIAXLEPPGAMA/VR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

```

CATTATTCCT TTTCCATCGG AAGTGGCGCT CGTGCATTCA ACTTGTTCCC GTCATGGAA    60
CCCCCTTTTA AAAAGACGCA GGGCACCTGT GAGCGCAGGA GCGAGCCTAA GGCCACCCAG    120
CGGCAGCGCC CGTGTCTTGG GCACTCAGCG TGCTGGGCAG AGCAGGTGCG ATG GSC      176
                               Met Xaa
CCA GTC CTA GCA GCC CTC GCC CAT GTC CTG TGC CCT TAC ATG GCT CCC      224
Pro Val Leu Ala Ala Leu Ala His Val Leu Cys Pro Tyr Met Ala Pro
      -35                -30                -25
GGA CTG TGC AGG GAG CCG ATA CGT TTK CTG ATA GCA VTA CTG GAA CCA      272
Gly Leu Cys Arg Glu Pro Ile Arg Xaa Leu Ile Ala Xaa Leu Glu Pro
      -20                -15                -10
CCG GGT GCG ATG GCA GTK AGG AGA CTG CCC AGT GCC                        308
Pro Gly Ala Met Ala Val Arg Arg Leu Pro Ser Ala
      -5                1                5

```

(2) INFORMATION FOR SEQ ID NO: 230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..309

id C16848
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 75..104
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 303..332
id R40385
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 73..207
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7
seq PMLGLAAFRWIWS/RE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

```

AAAAGCGGAC CCGCGGACGG TGGCGTTAAG GGAACGCTGA GGTCCCGCGC TCCCCGACCG      60
AGGTATATCT CC ATG AAT AAC CTA AAT GAT CCC CCA AAT TGG AAT ATC CGG      111
      Met Asn Asn Leu Asn Asp Pro Pro Asn Trp Asn Ile Arg
      -45                      -40                      -35

CCT AAT TCC AGG GCG GAT GGT GGT GAT GGA AGC AGG TGG AAT TAT GCC      159
Pro Asn Ser Arg Ala Asp Gly Gly Asp Gly Ser Arg Trp Asn Tyr Ala
      -30                      -25                      -20

CTG TTG GTT CCA ATG CTG GGA TTG GCT GCT TTT CGT TGG ATT TGG TCT      207
Leu Leu Val Pro Met Leu Gly Leu Ala Ala Phe Arg Trp Ile Trp Ser
      -15                      -10                      -5

AGG GAG TCC CAG AAA GAA GTA GAA AAA GAG AGA GAA GCC TAC CGT CGG      255
Arg Glu Ser Gln Lys Glu Val Glu Lys Glu Arg Glu Ala Tyr Arg Arg
      1                      5                      10                      15

AGA ACT GCT GCT TTT CAA CAG GAT CTG GAA GCC AAG TAC CAC GCC ATG      303
Arg Thr Ala Ala Phe Gln Gln Asp Leu Glu Ala Lys Tyr His Ala Met
      20                      25                      30

ATC TCA GAM AAT CGG CGT GCT GTC      327
Ile Ser Xaa Asn Arg Arg Ala Val
      35                      40

```

(2) INFORMATION FOR SEQ ID NO: 231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(3..297)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..295
id W57719
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(37..300)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 10..273
id H04979
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(7..41)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 270..304
id H04979
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(37..295)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 7..265
id H10390
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..41)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 262..301
id H10390
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(142..295)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..154
id W42765
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..141)
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 156..295
id W42765
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(55..238)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 71..254
id R39116
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(255..297)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 10..52
id R39116
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 295..351
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.6
seq AALCSLFFFLSLQ/EI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

```

ACGTTAGGGG GCCAGGGAGA TGTGACTGAG GCTGGCTTTC CACGTGAATG AGACGGGGTC   60
GGTGGAGGGT TTGGTGCTAC AGCCAGTCAG AAGATTGCA AATGCGAACA CATTCTGTG   120
TGAGGCACGT TACCCTTTGT CAGTTATTGT GAATATGTGT ATTTTAAGCA ATAAGATTCA   180
GCTGGTCAGA CTTTCTGGG CAGTCTCAGT GACGCATTTC CTGTGCTGTG ATTGTTCTGA   240
AGACAGAGTG GCTCTAACCA CTGTGAGAAG CCCAAATAAA AATTGATCCC AAAA ATG   297
                                         Met
CTA CTG CTC TTT CTT GCT GCA CTT TGT TCC CTC TTC TTC TTC CTC AGT   345
Leu Leu Leu Phe Leu Ala Ala Leu Cys Ser Leu Phe Phe Phe Leu Ser
      -15                      -10                      -5

CTT CAG GAA ATT GCA CCT CAA GAT CCC AAA CCA GGG   381
Leu Gln Glu Ile Ala Pro Gln Asp Pro Lys Pro Gly
      1                      5                      10

```

(2) INFORMATION FOR SEQ ID NO: 232:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 17..175
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 1..159
id W51023
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 42..173
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..132
id T61976
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 2..142
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.5
seq IIVCLFAFLVAHC/FL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

T ATG TTA TTC CTT GGC AAG GTG CTG ATA GTC TGC AGC ACA GGT TTA GCT	49
Met Leu Phe Leu Gly Lys Val Leu Ile Val Cys Ser Thr Gly Leu Ala	
-45 -40 -35	
GGG ATT ATG CTG CTC AAC TAC CAG CAG GAC TAC ACA GTA TGG GTG CTG	97
Gly Ile Met Leu Leu Asn Tyr Gln Gln Asp Tyr Thr Val Trp Val Leu	
-30 -25 -20	
CCT CTG ATC ATC GTC TGC CTC TTT GCT TTC CTA GTC GCT CAT TGC TTC	145
Pro Leu Ile Ile Val Cys Leu Phe Ala Phe Leu Val Ala His Cys Phe	
-15 -10 -5 1	
CTG TCT ATT TAT GAA ATG GTA GTK GAT GCG AGG	178
Leu Ser Ile Tyr Glu Met Val Val Asp Ala Arg	
5 10	

(2) INFORMATION FOR SEQ ID NO: 233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..321)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 59..378
id AA045815
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 95..244
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..150
id R18658
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 240..321
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 147..228
id R18658
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 95..321
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..227
id R14615
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..200)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 3..201
id N95174
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(36..197)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 8..169
id N93742
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..44)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 166..208
id N93742
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 191..304
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq LLLLVHSFWFTVC/TP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

```
AAGACTCATA GAGATTAAAT GATCACTATG GTCCTTCTTC TGTAAATGG AGCCAAAGAC      60
GCCTATGTTG TTCTGAAGTC TTGTAATGTT TAACTTCTGA GAACTTAGAT TAGTGGTGTG    120
ATGATAGAGT CTGTATAACG CATTGAAAAG GGTATCAGGC TTAGTTATTT ATCCAATAAA    180
TATTTATTGT ATG CAG GGT ATT CCT ATT TTA ACT CCT GTG ACA ACA CAA      229
      Met Gln Gly Ile Pro Ile Leu Thr Pro Val Thr Thr Gln
      -35                      -30

AGC ATA GCG ATT TCC ATA GTT CTA ACT GTT CAG GGT CTG CTC CTC CTG      277
Ser Ile Ala Ile Ser Ile Val Leu Thr Val Gln Gly Leu Leu Leu Leu
-25                      -20                      -15                      -10

GTA CAC TCT TTT TGG TTC ACT GTA TGT ACT CCT GTT GTC TTT              319
Val His Ser Phe Trp Phe Thr Val Cys Thr Pro Val Val Phe
      -5                      1                      5
```

(2) INFORMATION FOR SEQ ID NO: 234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(131..360)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 45..274
id M78402
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(57..234)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 10..187
id H04786
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(7..43)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 201..237
id H04786
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(57..234)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 10..187
id H17078
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(7..43)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 201..237
id H17078
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(57..217)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..161
id HSC0UC022
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..43)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 175..217
id HSC0UC022
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 199..279
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq LFCVLLSLRPHTS/GT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

```

ACAAGATTTT CCAACCTTGC TGGCTACTTT AGTTTGGGAC CTGTTTTTTT TCTCATTTGA    60
TTTTGCTTGT GCAGAAAATA GTTTCAGCA CATGGATTGA TCTGAGAGAG AATGAGGCTC    120
AGTTGTGGAT AGTCTGTTTT CTCTGAGCAT GTTGGCCAAC TAGTATCGTC AAATTATTGA    180
GTGGATCATC TCTTGGAA ATG CAG AAC TTC TGC CAC CAC TTG GCT ATT TGC    231
                Met Gln Asn Phe Cys His His Leu Ala Ile Cys
                -25                                -20

ACA GTC ATC TTG TTC TGT GTC CTT TTA TCT CTC AGA CCA CAC ACA TCT    279
Thr Val Ile Leu Phe Cys Val Leu Leu Ser Leu Arg Pro His Thr Ser
    -15                                -10                                -5

GGA ACG CTG TGG GCA TCT TCT GCC CAT GGG CTC CAT TTG GCA CCT GCT    327
Gly Thr Leu Trp Ala Ser Ser Ala His Gly Leu His Leu Ala Pro Ala
    1                                5                                10                                15

GAG CCA CAG TTG TCC TGC TGG ATG TGC TGT GCA    360
Glu Pro Gln Leu Ser Cys Trp Met Cys Cys Ala
                20                                25

```

(2) INFORMATION FOR SEQ ID NO: 235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 135..426
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 35..326
id H97426
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 92..316
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 14..238
id W44834
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 127..177
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 4..54
 id R57989
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 182..211
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 93
 region 62..91
 id R57989
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: complement(287..316)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 385..414
 id N93806
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 34..225
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.3
 seq VLMRLVASAYSIA/QK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

AAGTTTCCCG CATGCTCAGT AGCTGAGGTA GGG ATG CCA TCC TTC TCA AAA GAC	54
Met Pro Ser Phe Ser Lys Asp	
-60	
TTA TTG ACA GTG CCA AAG CTC GGT ACT GGA CAC VMC GRR GGR MCT GGG	102
Leu Leu Thr Val Pro Lys Leu Gly Thr Gly His Xaa Xaa Gly Xaa Gly	
-55 -50 -45	
TCC TAC GAT RAC GCG CTT KTG CTC CTC CTG AAG TGT CTT TGG TCC AAC	150
Ser Tyr Asp Xaa Ala Leu Xaa Leu Leu Lys Cys Leu Trp Ser Asn	
-40 -35 -30	
GTT GTT CCA GAG TGT ACC ATG GCT TCC AGT AAC ACT GTG TTG ATG CGG	198
Val Val Pro Glu Cys Thr Met Ala Ser Ser Asn Thr Val Leu Met Arg	
-25 -20 -15 -10	
TTG GTA GCC TCC GCA TAT TCT ATT GCT CAA AAG GCA GGA ATG ATA GTC	246
Leu Val Ala Ser Ala Tyr Ser Ile Ala Gln Lys Ala Gly Met Ile Val	
-5 1 5	
AGA CGT GTT ATT GCT GAA GGA GAC CTG GGT ATT GTG GAG AAG ACC TGT	294
Arg Arg Val Ile Ala Glu Gly Asp Leu Gly Ile Val Glu Lys Thr Cys	
10 15 20	
GCA ACA GAC CTG CAG ACC AAA GCT GAC CGA TTG GCA CAG ATG AGC ATA	342
Ala Thr Asp Leu Gln Thr Lys Ala Asp Arg Leu Ala Gln Met Ser Ile	

25	30	35	
TGT TCT TCA TTG GYM BGG AAA TTC CCC AAA CTC RNR ATT ATA GGG GAA			390
Cys Ser Ser Leu Xaa Xaa Lys Phe Pro Lys Leu Xaa Ile Ile Gly Glu			
40	45	50	55
GAG GAT CTG CCT TCT GAG GAA GTG GAT CAA GAG CTG ATT GAA GAC AGK			438
Glu Asp Leu Pro Ser Glu Glu Val Asp Gln Glu Leu Ile Glu Asp Xaa			
60	65	70	

(2) INFORMATION FOR SEQ ID NO: 236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 7..113
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 15..121
id W04921
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 114..220
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 121..227
id W04921
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 221..310
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 227..316
id W04921
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(114..213)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 260..359
id N70602
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(32..113)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 359..440
id N70602
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(261..311)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 164..214
id N70602
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(213..259)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 215..261
id N70602
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 114..194
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 59..139
id W70167
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 238..311
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 183..256
id W70167
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 55..113
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..59
id W70167
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 193..236
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 139..182

id W70167
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 221..311
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 165..255
id W37690
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 114..187
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 58..131
id W37690
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 56..113
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 1..58
id W37690
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 185..220
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 130..165
id W37690
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 227..289
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.2
seq LEMLXAFASHIXA/RD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

```
ATGGCAGCTT CCTTGGCTCG GCTTGGTCTG CGGCCTGTCA AACAGGTTCTG GGTTCAGTTC 60
TGTCCTTCG AGAAAAACGT GGAATCGACG AGGACCTTCV TSCAGACGGT GAGGCMGTGA 120
GAAGGTCCGC TCCAATAATC TCAACTGCTC AGTGATTGCG GACGTGASGC ATGACGGCTC 180
CGAGCCCTGC GTGGACGTGC TGTTCGGAGA CGGGCATCGC CTGATT ATG CGC GGC 235
                                     Met Arg Gly
                                     -20
GCT CAT CTC ACC GCT CTG GAA ATG CTC ANM GCC TTC GCC TCC CAC ATM 283
Ala His Leu Thr Ala Leu Glu Met Leu Xaa Ala Phe Ala Ser His Ile
```

-15

-10

-5

HGG GCC AGG GAC GCG GCG GGC AGC GGG
Xaa Ala Arg Asp Ala Ala Gly Ser Gly
1 5

310

(2) INFORMATION FOR SEQ ID NO: 237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 321..431
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 186..296
id AA043558
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 218..299
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 83..164
id AA043558
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 173..230
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 39..96
id AA043558
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 131..299
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 57..225
id N50523
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 321..431

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 247..357
id N50523
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(45..115)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..71
id N50523
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(321..431)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 289..399
id AA115605
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(217..318)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 403..504
id AA115605
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(166..231)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 491..556
id AA115605
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 172..318
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 36..182
id AA115129
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 321..431
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 186..296
id AA115129
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 174..318
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 41..185
 id AA035548
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 325..431
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 194..300
 id AA035548
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 7..423
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.2
 seq FGLLHQLSQCVTS/LE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

ACAAGG ATG GAA GTG GGC TTA CCG GCC ATT ACC CTC TTT CTC ACC AGC	48
Met Glu Val Gly Leu Pro Ala Ile Thr Leu Phe Leu Thr Ser	
-135 -130	
GCC AGC AGC CCT GTG GTG GCG ACG ACG ATG GAC CAG GAG CCA GTG GGC	96
Ala Ser Ser Pro Val Val Ala Thr Thr Met Asp Gln Glu Pro Val Gly	
-125 -120 -115 -110	
GGT GTG GAA CGA GGA GAA GCC GTC GCA GCC TCG GGA RCT GCG GCC GCC	144
Gly Val Glu Arg Gly Glu Ala Val Ala Ala Ser Gly Xaa Ala Ala Ala	
-105 -100 -95	
GCG GCA TTC GGG GAA TCT GCA GGG CAG ATG AGT AAC GAA AGA GGC TTT	192
Ala Ala Phe Gly Glu Ser Ala Gly Gln Met Ser Asn Glu Arg Gly Phe	
-90 -85 -80	
GAA AAT GTA GAA CTG GGA GTC ATA GGA AAA AAG AAG AAA GTC CCA AGG	240
Glu Asn Val Glu Leu Gly Val Ile Gly Lys Lys Lys Lys Val Pro Arg	
-75 -70 -65	
AGA GTC ATC CAC TTT GTT AGT GGT GAA ACA ATG GAA GAA TAT AGC ACA	288
Arg Val Ile His Phe Val Ser Gly Glu Thr Met Glu Glu Tyr Ser Thr	
-60 -55 -50	
GAT GAA GAC GAH GTT GAT GGC CTG GAG AAG NNG ATG TTT TGC CTA CTG	336
Asp Glu Asp Xaa Val Asp Gly Leu Glu Lys Xaa Met Phe Cys Leu Leu	
-45 -40 -35 -30	
TTG ATC CGR CAA AAC TTA CCT GGG GTC CCT ACT TAT GGT TTT ACA TGC	384
Leu Ile Arg Gln Asn Leu Pro Gly Val Pro Thr Tyr Gly Phe Thr Cys	
-25 -20 -15	
TTC GGG CTG CTA CAT CAA CTC TCT CAG TGT GTG ACT TCC TTG GAG	429
Phe Gly Leu Leu His Gln Leu Ser Gln Cys Val Thr Ser Leu Glu	

(2) INFORMATION FOR SEQ ID NO: 238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 102..322
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 31..251
id T34679
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 176..322
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 104..250
id N34677
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 93..170
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 21..98
id N34677
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 180..312
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 203..335
id N32531
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 180..312
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 202..334
id N36824

est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 102..170
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 28..96
 id N36824
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 175..312
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 100..237
 id H97539
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 151..279
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.1
 seq SAATLASLGGTSS/RR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

```

AACTCTCGTG CCAAGCATGT CTCTCCAAAT GGCTGCTCTC TGGCGTTCCT CACACTCCCC    60
CTGAAGTTCA TCTAAGATCT TCATTCTTCA WAGGCGGAAG CCCGGCTCGC TGCAAAACGG    120
GCGGCCCCGCG CGGAGGCTCG CGAGATCCGC ATG AAG GAG CTG GAG CGG CAG CAG    174
                               Met Lys Glu Leu Glu Arg Gln Gln
                               -40

AAG GAG GTA GAA GAG AGA CCA GAA AAA GAT TTT ACT GAG AAG GGG TCT    222
Lys Glu Val Glu Glu Arg Pro Glu Lys Asp Phe Thr Glu Lys Gly Ser
-35                -30                -25                -20

CGT AAC ATG CCG GGC CTG TCT GCA GCC ACG CTG GCC TCT CTG GGT GGG    270
Arg Asn Met Pro Gly Leu Ser Ala Ala Thr Leu Ala Ser Leu Gly Gly
          -15                -10                -5

ACT TCC TCT CGG AGA GGC AGC GGA GAC ACC TCC ATC TCC ATC GAC CCC    318
Thr Ser Ser Arg Arg Gly Ser Gly Asp Thr Ser Ile Ser Ile Asp Pro
          1                5                10

GAG    321
Glu

```

(2) INFORMATION FOR SEQ ID NO: 239:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 401 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 270..403
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 199..332
id AA125491
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 70..135
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 1..66
id AA125491
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(27..135)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 89..197
id HSB72F052
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(135..223)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 2..90
id HSB72F052
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 126..188
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.1
seq VLVILCIVTVCVT/IV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

```
ACCGGAGAAA AAATGGTTCA TGGAGCCTGC GGTTATTGTT TGCCTGGGTG GAATTTTACC   60
TTTTGGTTCA ATCTTTATTG AAATGTATTT CATCTTCACG TCTTTCTGGG CATATAAGAT  120
CTATT ATG TCT ATG GGC TTC ATG ATG CTG GTG CTG GTT ATC CTG TGC ATT   170
Met Ser Met Gly Phe Met Met Leu Val Leu Val Ile Leu Cys Ile
      -20                -15                -10
```

GTG ACT GTC TGT GTG ACT ATT GTG TGC ACA TAT TTT CTA CTA AAT GCA	218
Val Thr Val Cys Val Thr Ile Val Cys Thr Tyr Phe Leu Leu Asn Ala	
-5 1 5 10	
GAA GAT TAC AGG TGG CAA TGG ACA AGT TTT CTC TCT GCT GCA TCA ACT	266
Glu Asp Tyr Arg Trp Gln Trp Thr Ser Phe Leu Ser Ala Ala Ser Thr	
15 20 25	
GCA ATC TAT GTT TAC ATG TAT TCC TTT TAC TAC TAT TTT TTC AAA ACA	314
Ala Ile Tyr Val Tyr Met Tyr Ser Phe Tyr Tyr Tyr Phe Phe Lys Thr	
30 35 40	
AAG ATG TAT GGC TTA TTT CAA ACA TCA TTT TAC TTT GGA TAT ATG GCG	362
Lys Met Tyr Gly Leu Phe Gln Thr Ser Phe Tyr Phe Gly Tyr Met Ala	
45 50 55	
GTA TTT AGC ACA GCC TTG GGG ATA ATG TGT GGA GCG ATT	401
Val Phe Ser Thr Ala Leu Gly Ile Met Cys Gly Ala Ile	
60 65 70	

(2) INFORMATION FOR SEQ ID NO: 240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 153..397
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 131..375
id W56159
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..139
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..121
id W56159
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 153..467
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 303..617

id HSZ78368
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..139
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 214..293
id HSZ78368
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 153..374
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 80..301
id AA026570
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 70..139
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..70
id AA026570
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 372..405
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 300..333
id AA026570
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 155..467
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 83..395
id AA109961
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 88..139
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 20..71
id AA109961
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 153..363
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 96
region 274..484
id AA046907
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 60..139
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 185..264
id AA046907
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 128..337
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6
seq LLFPLTLVRSFWS/DM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

```

AACGCTTGCG ATGGTTGAAT TCCCCTCCTC ACGCCAGCCT AGGAGAAGAA GTTCGTAGTC      60
CCAGAGGAAG AGGAGTTGTA CGCATGTCAG AGAGGTTGCA GGCTGTTTTC AATTGTGTCAG    120
TTTGTTGG ATG ATG GAA TTG GRM CTW AAA AKC GRA ACT AAA KKG GAA TGK      169
      Met Met Glu Leu Xaa Leu Lys Xaa Xaa Thr Lys Xaa Glu Xaa
      -70                      -65                      -60
GAA TCT GCA TGT ACA GAA GCA TAT TCC CAA TCT GAT GAG CAA TAT GCT      217
Glu Ser Ala Cys Thr Glu Ala Tyr Ser Gln Ser Asp Glu Gln Tyr Ala
      -55                      -50                      -45
TGC CAT CTT GGT TGC CAG AAT CAG CTG CCA TTC GCT GAA CTG AGA CAA      265
Cys His Leu Gly Cys Gln Asn Gln Leu Pro Phe Ala Glu Leu Arg Gln
      -40                      -35                      -30                      -25
GAA CAA CTT ATG TCC CTG ATG CCA AAA ATG CAC CTA CTC TTT CCT CTA      313
Glu Gln Leu Met Ser Leu Met Pro Lys Met His Leu Leu Phe Pro Leu
      -20                      -15                      -10
ACT CTG GTG AGG TCA TTC TGG AGT GAC ATG ATG GAC TCC GCA CAG AGC      361
Thr Leu Val Arg Ser Phe Trp Ser Asp Met Met Asp Ser Ala Gln Ser
      -5                      1                      5
TTC AKA ACC TCT TCA TGG ACT TTT TAT CTT CAA GCC GAT GMC GGM MAA      409
Phe Xaa Thr Ser Ser Trp Thr Phe Tyr Leu Gln Ala Asp Xaa Gly Xaa
      10                      15                      20
ATA GTT ATA TKC CAG TCT AAG CCA GAA ATC CAG TAC GCA CCA CAT TTG      457
Ile Val Ile Xaa Gln Ser Lys Pro Glu Ile Gln Tyr Ala Pro His Leu
      25                      30                      35                      40
GAG CAG GAG
Glu Gln Glu

```

466

(2) INFORMATION FOR SEQ ID NO: 241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..81
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 62..125
id AA092155
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(18..81)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 68..131
id AA128307
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(18..81)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 68..131
id N99068
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(18..81)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 68..131
id AA039944
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(18..81)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 68..131
id AA128099
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide

- (B) LOCATION: 1..72
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6
seq GLILLFASHLINQ/FS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

ATG GTT TCC AAT GCT TCR GAG ACT TCC TGC CTA GGC CTC ATC CTC CTC	48
Met Val Ser Asn Ala Ser Glu Thr Ser Cys Leu Gly Leu Ile Leu Leu	
-20 -15 -10	
TTT GCC AGT CAC CTG ATT AAC CAA TTC TCC AGC	81
Phe Ala Ser His Leu Ile Asn Gln Phe Ser Ser	
-5 1	

(2) INFORMATION FOR SEQ ID NO: 242:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 373 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: DOUBLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Hypertrophic prostate
- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 29..302
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 99
region 1..274
id H18735
est
- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 143..302
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 100
region 116..275
id T80360
est
- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 79..143
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 92
region 51..115
id T80360
est
- (ix) FEATURE:
 - (A) NAME/KEY: other

(B) LOCATION: 29..69
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..41
id T80360
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 66..302
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..237
id AA137006
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 301..336
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 412..447
id AA137006
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 65..302
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 2..239
id HSC2CA081
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 64..224
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..161
id T36290
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 223..302
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 161..240
id T36290
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 2..220
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6
seq LIVFISVCTALLA/EG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

A ATG CCC CGG AAG CGG AAG TGC GAT CTT CGG GCT GTC AGA GTT GGT CTG	49
Met Pro Arg Lys Arg Lys Cys Asp Leu Arg Ala Val Arg Val Gly Leu	
-70 -65 -60	
TTA CTC GGT GGT GGC GGA GTC TAC GGA AGC CGT TTT CGC TTC ACT TTT	97
Leu Leu Gly Gly Gly Gly Val Tyr Gly Ser Arg Phe Arg Phe Thr Phe	
-55 -50 -45	
CCT GGC TGT AGA GCG CTT TCC CCC TGG CGG GTG AGA VTG CAG AGA CGA	145
Pro Gly Cys Arg Ala Leu Ser Pro Trp Arg Val Arg Xaa Gln Arg Arg	
-40 -35 -30	
AGG TGC GAG ATG AGC ACT ATG TTC GCG GAC ACT CTC CTC ATC GTT TTT	193
Arg Cys Glu Met Ser Thr Met Phe Ala Asp Thr Leu Leu Ile Val Phe	
-25 -20 -15 -10	
ATC TCT GTG TGC ACG GCT CTG CTC GCA GAG GGC ATA ACC TGG GTC CTG	241
Ile Ser Val Cys Thr Ala Leu Leu Ala Glu Gly Ile Thr Trp Val Leu	
-5 1 5	
GTT TAC AGG ACA GAC AAG TAC AAG AGA CTG AAG GCA GAA GTG GAA AAA	289
Val Tyr Arg Thr Asp Lys Tyr Lys Arg Leu Lys Ala Glu Val Glu Lys	
10 15 20	
CAG AGT AAA AAA TAT TTG ATG GTA GAG TGG TGG CAA ASC TTC CTT TTT	337
Gln Ser Lys Lys Tyr Leu Met Val Glu Trp Trp Gln Xaa Phe Leu Phe	
25 30 35	
TAC CCC TCT TTC TTA SAT CCA AAG RCT GTC TCA TCG	373
Tyr Pro Ser Phe Leu Xaa Pro Lys Xaa Val Ser Ser	
40 45 50	

(2) INFORMATION FOR SEQ ID NO: 243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 159..307
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 121..269
id W31320
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 37..121

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 1..85
id W31320
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 320..380
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 282..342
id W31320
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 114..165
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 77..128
id W31320
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 400..443
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 364..407
id W31320
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 154..307
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 2..155
id T27259
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 320..443
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 168..291
id T27259
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 192..307
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 108..223
id AA157646
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 64..95
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..32
id AA157646
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 320..443
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 123..246
id AA182962
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 198..307
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..110
id AA182962
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 243..307
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 189..253
id T71690
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 181..235
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 125..179
id T71690
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 114..164
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 58..108
id T71690
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 130..198
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq LGAAALALLANT/DV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

```

CCCCGCCCCCT GGGACCCTCC GGGCCGGGCG GTTGGCCCC TTAGCGCCCG GCGTCGGGG 60
CGGTAAAAGG CCGGCAGAAG GGAGGCACTT GAGAAATGTC TTCCTCCAG GACCCAAGTT 120
TTCTTCACC ATG GGG ATG TGG TCC ATT GGT GCA GGA GCC CTG GGG GCT GCT 171
      Met Gly Met Trp Ser Ile Gly Ala Gly Ala Leu Gly Ala Ala
            -20                      -15                      -10

GCC TTG GCA TTG CTG CTT GCC AAC ACA GAC GTG TTT CTG TCC AAG CCC 219
Ala Leu Ala Leu Leu Leu Ala Asn Thr Asp Val Phe Leu Ser Lys Pro
            -5                      1                      5

CAG AAA GCG GCC CTG GAG TAC CTG GAG GAT ATA GAC CTG AAA ACA CTG 267
Gln Lys Ala Ala Leu Glu Tyr Leu Glu Asp Ile Asp Leu Lys Thr Leu
            10                      15                      20

GAG AAG GAA CCA AGG ACT TTC AAA GCA AAG GAG CTA TGG GAA AAA AAT 315
Glu Lys Glu Pro Arg Thr Phe Lys Ala Lys Glu Leu Trp Glu Lys Asn
            25                      30                      35

GGA GCT GTG ATT ATG GCC GTG CGG AGG CCA GGC TGT TTC CTC TGT CGA 363
Gly Ala Val Ile Met Ala Val Arg Arg Pro Gly Cys Phe Leu Cys Arg
            40                      45                      50                      55

GAG GAA GCT GCG GAT CTG TCC TCC CTG AAA AGC ATG TTG GAC CAG CTG 411
Glu Glu Ala Ala Asp Leu Ser Ser Leu Lys Ser Met Leu Asp Gln Leu
            60                      65                      70

GGC GTC CCC CTC TAT GCA GTG GTA AAG GAG CAA CGG 447
Gly Val Pro Leu Tyr Ala Val Val Lys Glu Gln Arg
            75                      80

```

(2) INFORMATION FOR SEQ ID NO: 244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..382
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 13..394
id C17481
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 379..424
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 390..435
id C17481
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 68..258
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 72..262
id T46941
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 1..67
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 6..72
id T46941
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: complement(149..271)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 1..123
id R75331
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 257..430
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 42..215
id W95977
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 278..430
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 5..157
id R57521
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 255..347
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.9
seq LPLLLVANAGTAA/VG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

```

ATGAAAATGG GTGTGCTTAT TTCCACGAAG AGGAAAGAGA AGGACTTGCA AAGATATGTA    60
GGCTTGCCAT TCATTCTCGA TATGAAGACT TCGTAGTGGA TGGCTTCAAT GTGTTATATA    120
ACAAGAAGCC TGTCATATAT CTTAGTGCTG CTGCTAGACC TGGCCTGGGC CAATACCTTT    180
GTAATCAGCT CGGCTTGCCC TTCCCCTGCT TGTGCCGTGT ACCCTGTAAC ACTGTGTTTG    240
GATCCCAGCA TCAG ATG GAT GTT GCC TTC CTG GAG ADA CTG ATT AAA GAT    290
               Met Asp Val Ala Phe Leu Glu Xaa Leu Ile Lys Asp
               -30                      -25                      -20

GAT ATA GAG CGA GGA AGA CTG CCC CTG TTG CTT GTC GCA AAT GCA GGA    338
Asp Ile Glu Arg Gly Arg Leu Pro Leu Leu Leu Val Ala Asn Ala Gly
               -15                      -10                      -5

ACG GCA GCA GTA GGA CAC ACA GAC AAG ATT GGG AGA TTG AAA GAA CTC    386
Thr Ala Ala Val Gly His Thr Asp Lys Ile Gly Arg Leu Lys Glu Leu
               1                      5                      10

TGT GAG CAG TAT GGC ATA TGG CTT CAT GTG GAG GGT GTG AAT    428
Cys Glu Gln Tyr Gly Ile Trp Leu His Val Glu Gly Val Asn
    15                      20                      25

```

(2) INFORMATION FOR SEQ ID NO: 245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..230
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 3..232
id HSC1WH101
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 102..230
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 41..169
id R12437
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 63..104
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 1..42
 id R12437
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 63..230
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 1..168
 id R13448
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 165..212
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 36..83
 id T69236
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 180..227
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.8
 seq LFNLLWLALACSP/VW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

```

GTTTGTGGCC GTCCGGCCTC CCTGACATGC AGATTTCAC CCAGAAGACA GAGAAGGAGC   60
CAGTGGTCAT GGAATGGGCT GGGGTCAAAG ACTGGGTGCC TGGGAGCTGA GGCAGCCACC   120
GTTTCAGCCT GGCCAGCCCT CTGGACCCCG AGGTTGGACC CTACTGTGAC ACACCTACC   179
ATG CGG ACA CTC TTC AAC CTC CTC TGG CTT GCC CTG GCC TGC AGC CCT   227
Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro
  -15                -10                -5

GTT TGG                               233
Val Trp
1

```

(2) INFORMATION FOR SEQ ID NO: 246:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 330 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
(B) LOCATION: 178..331
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 118..271
id R60406
est

(ix) FEATURE:

- (A) NAME/KEY: other
(B) LOCATION: 178..316
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 57..195
id N78477
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 214..312
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.8
seq FICLQWALPHSEA/GD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

```

AAAGGCAGGA CTGACGCAGA ATGACAACGG CAACACGACA AGAAGTCCTT GGCCTCTACC   60
GCAGCATTTT CAGGCTTGCG AGGAAATGGC AGGCGACATC AGGGCAGATG GAAGACACCA   120
TCAAAGAAAA ACAGTACATA CTAAATGAAG CCAGAACGCT GTTCCGGAAA AACAAAAATC   180
TCACGGACAC AGACCTAATT AAACAGTGTA TAG ATG AAT GCA CAG CCA GGA TTG   234
                Met Asn Ala Gln Pro Gly Leu
                -30

AWA TTG GAC TGC ATT ACA AGA TTC CTT ACC CAN GGC CAA TTC ATC TGC   282
Xaa Leu Asp Cys Ile Thr Arg Phe Leu Thr Xaa Gly Gln Phe Ile Cys
-25                -20                -15

CTC CAA TGG GCC TTA CCC CAC TCC GAG GCC GGG GAC TTC GAA GCC AAG   330
Leu Gln Trp Ala Leu Pro His Ser Glu Ala Gly Asp Phe Glu Ala Lys
-10                -5                1                5

```

(2) INFORMATION FOR SEQ ID NO: 247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(230..352)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 32..154
id W60134
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(78..189)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 195..306
id W60134
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(9..87)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 298..376
id W60134
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(176..352)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 57..233
id H64097
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(57..189)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 219..351
id H64097
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(84..352)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 57..325
id W00624
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: complement(1..70)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 337..406
id W00624
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(1..168)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 156..323
id W67127
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(167..323)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 2..158
id W67127
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(64..352)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 58..346
id H10776
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(23..64)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 347..388
id H10776
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 120..326
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.7
seq LCRLCLVRLFCC/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

```
ATTGGGGGAG GGGCACTGTC TCTTTTTTCT CTCATTTTTA AAATGAAGTG TTGTTGCCTT    60
TGTATGTGGT TCAACCATCC AGCTCCCAGC TGGCTAAACT TTGCCTCCAG TGGTCAAAG    119
ATG GGA AAA GAG TGG GGT TGG CAG GAG ATG GAA AAC GGA GGT GCC GCC    167
Met Gly Lys Glu Trp Gly Trp Gln Glu Met Glu Asn Gly Gly Ala Ala
      -65                      -60                      -55
```

CCA GCA TGG GGG GCA GGT CCC CCA GTC CAC CCT GCC CCT CCC CCT GTG	215
Pro Ala Trp Gly Ala Gly Pro Pro Val His Pro Ala Pro Pro Pro Val	
-50 -45 -40	
GAG AAG ACG CTT AGT TGG GGG TGT GGG TTT GGG CTC CAT TCT GGA TTC	263
Glu Lys Thr Leu Ser Trp Gly Cys Gly Phe Gly Leu His Ser Gly Phe	
-35 -30 -25	
GGC GGT TCC GGG GGA GGG GTG GGT CTG TGC CGA TTA CTC TGT CTT GTA	311
Gly Gly Ser Gly Gly Gly Val Gly Leu Cys Arg Leu Leu Cys Leu Val	
-20 -15 -10	
CGT TTG TTC TGC TGC TCT TCA ATA TTG TAT CAA CGC CAG AAG	353
Arg Leu Phe Cys Cys Ser Ser Ile Leu Tyr Gln Arg Gln Lys	
-5 1 5	

(2) INFORMATION FOR SEQ ID NO: 248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..71
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 1..50
id R82719
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..62
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 1..44
id AA069083
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 20..52
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 2..34
id R29193
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 23..52
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 10..39
id AA158081
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 10..96
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.7
seq AALLLTATVRLSA/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

AAGTCCAAC ATG GCG GCG CCC AGC GGA GGG TGG AAC GGC GTC GGC GCG AGC 51
Met Ala Ala Pro Ser Gly Gly Trp Asn Gly Val Gly Ala Ser
-25 -20

TTG TGG GCC GCG CTG CTC CTC ACT GCC ACA GTC AGA CTT TCA GCT TCT 99
Leu Trp Ala Ala Leu Leu Leu Thr Ala Thr Val Arg Leu Ser Ala Ser
-15 -10 -5 1

CCC GGC CCA 108
Pro Gly Pro

(2) INFORMATION FOR SEQ ID NO: 249:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 393 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 7..165
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..159
id R24141
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 178..264
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 173..259
id R24141
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 258..299
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 254..295
id R24141
est

(ix) FEATURE:

[illegible]

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 4..147
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.7
seq LLLFFGKLLVVGG/VG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

ATC	ATG	ATC	GCC	ATC	TAC	GGG	AAG	AAT	TTC	TGT	GTC	TCA	GCC	AAA	AAT	48
Met	Ile	Ala	Ile	Tyr	Gly	Lys	Asn	Phe	Cys	Val	Ser	Ala	Lys	Asn		
			-45					-40						-35		
GCG	TTC	ATG	CTA	CTC	ATG	CGA	AAC	ATT	GTC	AGG	GTG	GTC	GTC	CTG	GAC	96
Ala	Phe	Met	Leu	Leu	Met	Arg	Asn	Ile	Val	Arg	Val	Val	Val	Leu	Asp	
			-30					-25						-20		
AAA	GTC	ACA	GAC	CTG	CTG	CTG	TTC	TTT	GGG	AAG	CTG	CTG	GTG	GTC	GGA	144
Lys	Val	Thr	Asp	Leu	Leu	Leu	Phe	Phe	Gly	Lys	Leu	Leu	Val	Val	Gly	
		-15					-10						-5			
GGC	GTG	GGG	GTC	CTG	TCC	TTC	TTT	TTT	TTC	TCC	GGT	CGC	ATC	CCG	GGG	192
Gly	Val	Gly	Val	Leu	Ser	Phe	Phe	Phe	Phe	Ser	Gly	Arg	Ile	Pro	Gly	
	1				5					10					15	
CTG	GGT	AAA	GAC	TTT	AAG	AGC	CCC	CAC	CTC	AAC	TAT	TAC	TGG	CTG	CCC	240
Leu	Gly	Lys	Asp	Phe	Lys	Ser	Pro	His	Leu	Asn	Tyr	Tyr	Trp	Leu	Pro	
				20				25						30		
AYC	ATG	ACC	TCC	ATC	CTG	GGG	GCC	TAT	GTC	ATC	GCC	AGY	GGC	TTC	TTC	288
Xaa	Met	Thr	Ser	Ile	Leu	Gly	Ala	Tyr	Val	Ile	Ala	Ser	Gly	Phe	Phe	
			35					40					45			
AGC	GTT	TTC	GGC	ATG	TGT	GTG	GAC	ACG	CTC	TTC	CTC	TGC	TTC	CTG	GAA	336
Ser	Val	Phe	Gly	Met	Cys	Val	Asp	Thr	Leu	Phe	Leu	Cys	Phe	Leu	Glu	
		50					55					60				
GAC	CTG	GAG	CGG	ACA	ACG	GCT	CCC	TGG	ACG	GCC	CTA	CTA	CAT	GTC	CAA	384
Asp	Leu	Glu	Arg	Thr	Thr	Ala	Pro	Trp	Thr	Ala	Leu	Leu	His	Val	Gln	
	65					70					75					

GAG CTT CTA
Glu Leu Leu
80

393

(2) INFORMATION FOR SEQ ID NO: 250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 222..265
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 220..263
id N89186
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 76..348
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7
seq SVLELIVASVCQS/HI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

```

GCTACTTTCT TTTTCAGTCT TTCGGTGCGG AGAAGGGGAG GAGGCGGGCA GAGGTCTGAA   60
AAAATCGAAT GCCTT ATG GAA AGG AAC TGC AAG GGT TCC TTT GGG GTG ATC   111
      Met Glu Arg Asn Cys Lys Gly Ser Phe Gly Val Ile
      -90                      -85                      -80

AAA GAG GGA GAC ACA GAC ACA GRR GAG ACA AAG GCA AGG AGG ACT GTC   159
Lys Glu Gly Asp Thr Asp Thr Xaa Glu Thr Lys Ala Arg Arg Thr Val
      -75                      -70                      -65

TGG GAG CCA CGC GGG CGA TAC AGT TTC CGA GRM ACG CCG CGT CCC GCC   207
Trp Glu Pro Arg Gly Arg Tyr Ser Phe Arg Xaa Thr Pro Arg Pro Ala
      -60                      -55                      -50

TAT CCT GTT GAA CAG TGC GGA TTT GCG AGG CGC GCC CTG GAG CTG CTA   255
Tyr Pro Val Glu Gln Cys Gly Phe Ala Arg Arg Ala Leu Glu Leu Leu
      -45                      -40                      -35

GAG ATC CGG AAG CAC AGC CCC GAG GTG TGC GAA CCA CCA AAC ATC CCA   303
Glu Ile Arg Lys His Ser Pro Glu Val Cys Glu Pro Pro Asn Ile Pro
      -30                      -25                      -20

```

GTT ACC AGT GTC CTT GAA TTG ATA GTG GCT TCT GTT TGT CAG TCT CAT 351
 Val Thr Ser Val Leu Glu Leu Ile Val Ala Ser Val Cys Gln Ser His
 -15 -10 -5 1

ATA AGA ACT ACT 363
 Ile Arg Thr Thr
 5

(2) INFORMATION FOR SEQ ID NO: 251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..264
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..243
id AA211459
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 15..212
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7
seq LYMLAEALPVSHG/AH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

GTGAAGATGA AGCC ATG TTT GTA GAA TAT AGA AAA CAA CTG AAG TTA CTG 50
 Met Phe Val Glu Tyr Arg Lys Gln Leu Lys Leu Leu
 -65 -60 -55

TTG GAC AGG CTT GCT CAA GTT TCA CCA GAG TTA CTA CTG GCC TCT GTT 98
 Leu Asp Arg Leu Ala Gln Val Ser Pro Glu Leu Leu Leu Ala Ser Val
 -50 -45 -40

CGC AGA GTT TTT AGT TCT ACA CTG CAG AAT TGG CAG ACT ACA CGG TTT 146
 Arg Arg Val Phe Ser Ser Thr Leu Gln Asn Trp Gln Thr Thr Arg Phe
 -35 -30 -25

ATG GAA GTT GAA GTA GCA ATA AGA TTG CTG TAT ATG TTG GCA GAA GCT 194
 Met Glu Val Glu Val Ala Ile Arg Leu Leu Tyr Met Leu Ala Glu Ala
 -20 -15 -10

CTT CCA GTA TCT CAT GGT GCT CAC TTC TCA GGT GAT GTT TCA AAA GCT 242
 Leu Pro Val Ser His Gly Ala His Phe Ser Gly Asp Val Ser Lys Ala

-5	1	5	10	
AGT GCT TTG CAG GAT ATG ATG CGA ACT CTG GTA ACA TCA GGA GTC AGC				290
Ser Ala Leu Gln Asp Met Met Arg Thr Leu Val Thr Ser Gly Val Ser				
	15	20	25	
GGG				293
Gly				

(2) INFORMATION FOR SEQ ID NO: 252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 155..187
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 95..127
id H83489
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 326..388
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7
seq IIFLIQWHGSVFQ/EF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

AAGTCCCTGT ACAGGGTTTC TGACCTGTGG TAAAAACAGA ATGTCACTTT CTGACAGGCA	60
CAGTACCCCC AGGATAAACT TGGAACCTCG AGAGGAAATT CACGAACTC GTGGGGGCAG	120
GGGTCACAAG GTGCTTGGTG GGGGARAASC TGGAAGACAT ATTGTCCAGG AGAAGGAATG	180
TCACAAGGAA CTGACAAAAT CAAGTCACGG CGCCTACAAA GATGAGGGGC AGATTCTGGC	240
TGCCTTTTAA TTTCGTCCTT CACCTGATAT CTGTGCCAGA GAATGATAAA AATCATAATA	300
AAGGRAATAG YGGAAGAGGA GACTT ATG TTA CTG GGG ACA TCT AAC ATA ATT	352
Met Leu Leu Gly Thr Ser Asn Ile Ile	
-20 -15	
ATT TTC CTG ATT CAG TGG CAT GGT TCA GTC TTC CAG GAG TTC	394
Ile Phe Leu Ile Gln Trp His Gly Ser Val Phe Gln Glu Phe	
-10 -5 1	

(2) INFORMATION FOR SEQ ID NO: 253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 48..238
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 35..225
id HSC0CC021
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 15..49
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 1..35
id HSC0CC021
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 27..238
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..212
id T32119
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 36..238
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..203
id T35494
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 49..238
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 13..202
id HUMHG5097
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 51..238
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..188
id AA027882
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 78..137
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq AFVXACVLSLIST/IY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

```

AAGAGTAGGG TGCTGTGGTC TGAGCTAGAG GGTGAAGCTG GCGGASAGGA GGATGGGCGA    60
GCAGTCTGAA TGCCAGA ATG GRT AAC CGT TTT GCT ACA GCA TTT GTA ATD    110
      Met Xaa Asn Arg Phe Ala Thr Ala Phe Val Xaa
      -20                      -15                      -10
GCT TGT GTG CTT AGC CTC ATT TCC ACC ATC TAC ATG GCA GCC TCC ATT    158
Ala Cys Val Leu Ser Leu Ile Ser Thr Ile Tyr Met Ala Ala Ser Ile
      -5                      1                      5
GGC ACA GAC TTC TGG TAT GAA TAT CGA AGT CCA GTT CAA GAA AAT TCC    206
Gly Thr Asp Phe Trp Tyr Glu Tyr Arg Ser Pro Val Gln Glu Asn Ser
      10                      15                      20
AGT GAT TTG AAT AAA AGC ATC TGG GAT GAA TTG    239
Ser Asp Leu Asn Lys Ser Ile Trp Asp Glu Leu
      25                      30

```

(2) INFORMATION FOR SEQ ID NO: 254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(43..130)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 176..263
id C01485

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(137..219)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 88..170
id C01485
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 421..459
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq MSLTSGFLRVSQG/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

```

CACCAATGTT ATGAATGGCG TGGCCTCCTA CTGCCGTCCC TGTGCCCTAG AAGCCTCTGA    60
TGTGGGCTCC TCCTGCACCT CTTGTCCTGC TGGTTACTAT ATTGACCGAG ATTCAGGAAC    120
CTGCCAMTCC BTGCCCCCCT AACACAATTC TGAAAGCCCA CCAGCCTTAT GGTGTCCAGG    180
CCTGTGTGCC CTGTGGTCCA GGGACCAAGA ACAACAAGAT CCACTCTCTG TGCTACAATG    240
ATTGCACCTT CTCACGCAAC ACTCCAACCA GGACTTTCAA CTACAACTTC TCCGCTTTGG    300
CAAACACCGT CACTCTTGCT GGAGGGCCAA GCTTCACTTC CAAAGGGTTG AAATACTTCC    360
ATCACTTTAC CCTCAGTCTC TGTGGAAACC AGGGTAGGAA AATGTCTGTG TGCACCGACA    420
ATG TCA CTG ACC TCC GGA TTC CTG AGG GTG AGT CAG GGT TCT CCA AAT    468
Met Ser Leu Thr Ser Gly Phe Leu Arg Val Ser Gln Gly Ser Pro Asn
      -10                -5                1

CTA TCA CAG                                477
Leu Ser Gln
  5 -

```

(2) INFORMATION FOR SEQ ID NO: 255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 55..316
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..262
id H87671
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 102..261
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 50..209
id N47067
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 55..104
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 2..51
id N47067
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 251..316
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 14..79
 id AA135001
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 58..246
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.6
seq AIRTLSVTGILA/EO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

AACTTGGCGC	GCGGSSGGC	TGCAGACGGC	TGCGAGGCGC	TGGGCACAGG	TGTCCTG	57
ATG GCA AAT TTC AAG GGC CAC GCG CTT CCA GGG AGT TTC TTC CTG ATC	105					
Met Ala Asn Phe Lys Gly His Ala Leu Pro Gly Ser Phe Phe Leu Ile						
-60 -55 -50						
ATT GGG CTG TGT TGG TCA GTG AAG TAC CCG CTG AAG TAC TTT AGC CAC	153					
Ile Gly Leu Cys Trp Ser Val Lys Tyr Pro Leu Lys Tyr Phe Ser His						
-45 -40 -35						
ACG CGG AAG AAC AGC CCA CTA CAT TAC TAT CAG CGT CTC GAG ATC GTC	201					
Thr Arg Lys Asn Ser Pro Leu His Tyr Tyr Gln Arg Leu Glu Ile Val						
-30 -25 -20						
GAA GCC GCA ATT AGG ACT TTG TTT TCC GTC ACT GGG ATC CTG GCA GAG	249					
Glu Ala Ala Ile Arg Thr Leu Phe Ser Val Thr Gly Ile Leu Ala Glu						
-15 -10 -5 1						

CAG TTT GTT CCG GAT GGG CCC CAC CTG CAC CTC TAC CAT GAG AAC CAC 297
Gln Phe Val Pro Asp Gly Pro His Leu His Leu Tyr His Glu Asn His
5 10 15
TGG ATA AAG TTA ATG AAT 315
Trp Ile Lys Leu Met Asn
20

(2) INFORMATION FOR SEQ ID NO: 256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 89..405
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 84..400
id N34255
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 5..88
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..84
id N34255
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 89..304
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 83..298
id H79944
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 8..54
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 2..48
id H79944
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 336..382
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 332..378
id H79944
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 304..340
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 299..335
id H79944
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 54..88
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 49..83
id H79944
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 109..298
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 106..295
id H73369
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..88
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 1..87
id H73369
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 336..382
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 336..382
id H73369
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 295..326
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 293..324
id H73369

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 164..237
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 142..215
id AA132425
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 327..395
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 307..375
id AA132425
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 21..88
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 3..70
id AA132425
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 124..163
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 103..142
id AA132425
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 109..298
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 24..213
id R97376
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 296..405
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 212..321
id R97376
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 187..342
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5

seq AGLLFGSLAGLGA/YQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

```

AGCAGGCACA ACAGAGCCGC TCCCCWCTCC TCGCCCCGCC ACCGGGACGG AGAGCGCCCG 60
CCGCTGCATT TCCGGCGACA CCTCGCAGGT CATTCTGCG GCTTGCGCGC CCTTGTAGAC 120
AGCCGGGGCC TTCGTSAGAC CGGTGCAGGC CTGGGGTAGT CTCCTGTCTG GACAGAGAAG 180
AGAAAA ATG CAG GAC ACT GGC TCA GTA GTG CCT TTG CAT TGG TTT GGC 228
      Met Gln Asp Thr Gly Ser Val Val Pro Leu His Trp Phe Gly
            -50                -45                -40

TTT GGC TAC GCA GCA CTG GTT GCT TCT GGT GGG ATC ATT GGC TAT GTA 276
Phe Gly Tyr Ala Ala Leu Val Ala Ser Gly Gly Ile Ile Gly Tyr Val
      -35                -30                -25

AAA GCA GGC AGC GTG CCG TCC CTG GCT GCA GGG CTG CTC TTT GGC AGT 324
Lys Ala Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser
      -20                -15                -10

CTA GCC GGC CTG GGT GCT TAC CAG CTG TCT CAG GAT CCA AGG AAC GTT 372
Leu Ala Gly Leu Gly Ala Tyr Gln Leu Ser Gln Asp Pro Arg Asn Val
      -5                1                5                10

TGG GTT TTC CTA GCT ACA TCT GGT ACC TTG GCT 405
Trp Val Phe Leu Ala Thr Ser Gly Thr Leu Ala
            15                20

```

(2) INFORMATION FOR SEQ ID NO: 257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 119..237
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 116..234
id HSC2TH021
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 25..95
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94

region 24..94
id HSC2TH021
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 238..289
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 234..285
id HSC2TH021
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 280..319
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 277..316
id HSC2TH021
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 130..237
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 23..130
id R59681
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 238..289
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 130..181
id R59681
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 280..325
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 173..218
id R59681
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 183..287
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.4
seq CCALLTSLXCIWG/PA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

ACCTTCTGTT ACTGTCCGGG GCTGCGGGG TTGCTTCCKG CGTCAWGGCT CAAAGGGCCT 60


```

TCCCGMATCC TTATGCTGAT TATAACAAAT CCCTGDRCCG AAGSTACTTT GATGCTGCCG 120
GGARGCTGAC TCCTGAGTTC TCACAACGCT TGACCAATAA GATTCGGGAG CTTCTTCAGC 180
AA ATG GAG AKA GGC CTG AAA TCA GCA GAC CCT CGG GAT GGC ACC GGT 227
  Met Glu Xaa Gly Leu Lys Ser Ala Asp Pro Arg Asp Gly Thr Gly
   -35                -30                -25
TAC ACT GRC TTN NKC ARG TAT TGC TGT GCT TTA CTT ACA TCT TTA TGR 275
Tyr Thr Xaa Xaa Xaa Xaa Tyr Cys Cys Ala Leu Leu Thr Ser Leu Xaa
  -20                -15                -10                -5
TGT ATT TGG GGA CCT GCC TAC CTA CAG TTA GCA CAT GGC TAT GTA AAG 323
Cys Ile Trp Gly Pro Ala Tyr Leu Gln Leu Ala His Gly Tyr Val Lys
          1                5                10

```

(2) INFORMATION FOR SEQ ID NO: 258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..241
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 12..252
id H64050
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..241
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..241
id R17172
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..241
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 2..242
id HSC15C081
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 8..241
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..234
id AA149663
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 29..241
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 29..241
id HSU46380
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 10..135
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.4
seq ITGVILLAVGIWG/KV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

GGGCTAGTC ATG GCG TCC CCG TCT CGG AGA CTG CAG ACT AAA CCA GTC ATT	51
Met Ala Ser Pro Ser Arg Arg Leu Gln Thr Lys Pro Val Ile	
-40 -35 -30	
ACT TGT TTC AAG AGC GTT CTG CTA ATC TAC ACT TTT ATT TTC TGG ATC	99
Thr Cys Phe Lys Ser Val Leu Leu Ile Tyr Thr Phe Ile Phe Trp Ile	
-25 -20 -15	
ACT GGC GTT ATC CTT CTT GCA GTT GGC ATT TGG GGC AAG GTG AGC CTG	147
Thr Gly Val Ile Leu Leu Ala Val Gly Ile Trp Gly Lys Val Ser Leu	
-10 -5 1	
GAG AAT TAC TTT TCT CTT TTA AAT GAG AAG GCC ACC AAT GTC CCC TTC	195
Glu Asn Tyr Phe Ser Leu Leu Asn Glu Lys Ala Thr Asn Val Pro Phe	
5 10 15 20	
GTG CTC ATT GCT ACT GGT ACC GTC ATT ATT CTT TTG GGC ACC TTG	240
Val Leu Ile Ala Thr Gly Thr Val Ile Ile Leu Leu Gly Thr Leu	
25 30 35	

(2) INFORMATION FOR SEQ ID NO: 259:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 385 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 8..349
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 6..347
id AA075824
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 344..385
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 341..382
id AA075824
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..366
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 2..346
id R55598
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 71..385
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..315
id HSC33B061
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 156..385
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 91..320
id T65515
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 70..141
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 5..76
id T65515
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 29..305
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 2..278

id HSCZRF061
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 119..319
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2
seq LSVSLLPCAGAWS/LL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

```
AAAAGCGGAG MYAGGMNGGG TGAGGAGAGT CGAGGGAGGT GACGCGCGCT GCCGGGGCGA    60
GGTTGCGAGG GCGGGTGTG AAGAATGTGT GGGCGAACAT CCTGTCACTT ACCTAGAG    118
ATG TTC TCA CGA GAG CTT GCG CCT ACC AGG ATC GGC GGG GCC AGC AGC    166
Met Phe Ser Arg Glu Leu Ala Pro Thr Arg Ile Gly Gly Ala Ser Ser
      -65                      -60                      -55
GGC TCC CGG AGT GGA GGG ACC CTG ATA AGT ACT GCC CCT CTT ACA ACA    214
Gly Ser Arg Ser Gly Gly Thr Leu Ile Ser Thr Ala Pro Leu Thr Thr
      -50                      -45                      -40
AGA GTC CTC AAT CCA ACA GCC CAG TGC TTC TGT CTC GAC TGC ACT TTG    262
Arg Val Leu Asn Pro Thr Ala Gln Cys Phe Cys Leu Asp Cys Thr Leu
      -35                      -30                      -25                      -20
AGA AGG ATG CAG ACT CAT CTG AGC GTA TCA TTG CTC CCA TGC GCT GGG    310
Arg Arg Met Gln Thr His Leu Ser Val Ser Leu Leu Pro Cys Ala Gly
      -15                      -10                      -5
GCT TGG TCC CTT CTT RGT TCA AAG AAA GTG ATC CTT CCA AGC TGC AGT    358
Ala Trp Ser Leu Leu Xaa Ser Lys Lys Val Ile Leu Pro Ser Cys Ser
      1                      5                      10
TCA ATA CTA MCA ACT GTC GTA GTG ATA    385
Ser Ile Leu Xaa Thr Val Val Val Ile
      15                      20
```

(2) INFORMATION FOR SEQ ID NO: 260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 43..128
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97
region 19..104
id R49759
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 132..194
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 106..168
id R49759
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 225..311
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.1
seq LLMLGVTLPSYW/RV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

```

ATTCCTCTGA CCTGCCAGGA AGCAGAGAGA CCCACAGAGC AGGCAGGGAG GCAGAAAGTG   60
GAGACGGACC TGAGCCCGAG GAAGAGGCAG GCAGAGGCTG AGGCTGATTC CACCCAGACC   120
TGCCTGGRAC AAACCCTCCT TAGCCGCAGC CCCTTCCAGT TCCCTAGGGG TTCTGCCCCCT   180
CCCCCTCTCT GGGGCACCAG CCCCCAGGG TCCTGCATCC NACC ATG TCG ATG GCT   236
                               Met Ser Met Ala
GTG GAA ACC TTT GGC TTC TTC ATG GCA ACT GTG GGG CTG CTG ATG CTG   284
Val Glu Thr Phe Gly Phe Phe Met Ala Thr Val Gly Leu Leu Met Leu
-25                -20                -15                -10
GGG GTG ACT CTG CCA AAC AGC TAC TGG CGA GTG TCC ACT GTG CAC GGG   332
Gly Val Thr Leu Pro Asn Ser Tyr Trp Arg Val Ser Thr Val His Gly
                -5                1                5
AAC GTC ATC AHC ACC AAC AHC ATC TTC GAG AAC CTC TGG TTT AGC AGT   380
Asn Val Ile Xaa Thr Asn Xaa Ile Phe Glu Asn Leu Trp Phe Ser Ser
                10                15                20
GCC GGG
Ala Gly
25

```

(2) INFORMATION FOR SEQ ID NO: 261:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 222 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 118..222
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 112..216
id T86663
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 118..156
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 120..158
id AA055880
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 55..114
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq XFLXLXXLSXXWP/XD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

```

ACTCAGAAGC TTGGACCGCA TCCTAGCCGC CGACTCACAC AAGGCAGABT TGCC ATG      57
                                     Met
                                     -20

GAG AAA ATT CCA GTG TCA SCA TTC TTG CDC CTN GYG GSC CTC TCK WAS      105
Glu Lys Ile Pro Val Ser Xaa Phe Leu Xaa Leu Xaa Xaa Leu Ser Xaa
      -15                      -10                      -5

AKC TGG CCA SSG GAT ACC ACA GTC AAA CCT GGA GCC AMA AAG GAC ACA      153
Xaa Trp Pro Xaa Asp Thr Thr Val Lys Pro Gly Ala Xaa Lys Asp Thr
      1                      5                      10

AAG GAC TCT CGA SCC AAA CTG CCC CAG ACC CTC TCC AGA GGT TGG GGT      201
Lys Asp Ser Arg Xaa Lys Leu Pro Gln Thr Leu Ser Arg Gly Trp Gly
      15                      20                      25

GAC CAA CTC ATC TGG ACA CGG      222
Asp Gln Leu Ile Trp Thr Arg
      30                      35

```

(2) INFORMATION FOR SEQ ID NO: 262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 207..326

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98
region 85..204
id W69716
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 122..208

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97
region 1..87
id W69716
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 316..366

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 94
region 195..245
id W69716
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 282..366

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 94..178
id W73842
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 207..287

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98
region 17..97
id W73842
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 257..326

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 94
region 42..111
id W58108
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 317..366
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 101..150
id W58108
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 112..312
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq LILERPLVPSAEA/SG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

```

ATAAGGCCTC AGGGTCCTGT TTTCCCTGGC CTCTTCTAGA GGGCCCGTGG AMCAGGTGCG 60
AGTGCGTGCT TATTTGGAAG CCAGGTGTGT GAGCCGAATG CCTGCCAGGC C ATG CAC 117
                                         Met His

TCA GCA GAG GAG CCC TTG TAN CTG GCT GCC CTG AGA GGA GCA AGA GGC 165
Ser Ala Glu Glu Pro Leu Xaa Leu Ala Ala Leu Arg Gly Ala Arg Gly
-65                -60                -55                -50

CAC CTC CCA TGT GGC TCT AGA CAC CAC GTG GGC TCA TTA GCC CCA GCG 213
His Leu Pro Cys Gly Ser Arg His His Val Gly Ser Leu Ala Pro Ala
                -45                -40                -35

TCT GTG CCG GCT CCA GGT GCC TGC CTC TGG GTG TGT GAG TGG GAG ACT 261
Ser Val Pro Ala Pro Gly Ala Cys Leu Trp Val Cys Glu Trp Glu Thr
                -30                -25                -20

TTG CTC CCT GGC CTC ATC CTA GAG AGG CCC CTG GTG CCT AGT GCT GAG 309
Leu Leu Pro Gly Leu Ile Leu Glu Arg Pro Leu Val Pro Ser Ala Glu
                -15                -10                -5

GCC TCT GGG GCT GGA AAG CTC AGC AGA AAG GAG GCA CTA CTG AGC AAC 357
Ala Ser Gly Ala Gly Lys Leu Ser Arg Lys Glu Ala Leu Leu Ser Asn
      1                5                10                15

TAT GCA TTG
Tyr Ala Leu 366

```

(2) INFORMATION FOR SEQ ID NO: 263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 121..264
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 127..270
id N24991
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 3..124
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 10..131
id N24991
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 161..292
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 15..146
id HSC1WG111
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 176..310
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..135
id AA001396
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 176..265
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..90
id AA017578
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 191..265
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..75
id R17530
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 167..295
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.9

seq GLWLALVDGLVRX/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

```

ACTTTTTCCT ACGCAGCCGC TCCTGCCGCC GTGGTCGCTG GAGCTTTGCC TCTCTAGGCC   60
GGCAGCGCCT CTCCTCCATG GTCCTGTCTG TCAGCGCTGT TTTGGGAGCC CGCCGGTGAG  120
GCCGGGCCAC GCTCAGACAC TTCGATCGTC GAGTCTGTCA CTGGGC ATG GCG GGT   175
                               Met Ala Gly
CAG TTC CGC AGC TAC GTG TGG GAC CCG CTG CTG ATC CTG TCG CAG ATC   223
Gln Phe Arg Ser Tyr Val Trp Asp Pro Leu Leu Ile Leu Ser Gln Ile
-40                -35                -30                -25

GTC CTC ATG CAG ACC GTG TAT TAC GGC TCG CTG GGC CTG TGG CTG GCG   271
Val Leu Met Gln Thr Val Tyr Tyr Gly Ser Leu Gly Leu Trp Leu Ala
                -20                -15                -10

CTG GTG GAC GGG CTA GTG CGA ASA GCC CCT CGC TGG ATC SCA GGG   316
Leu Val Asp Gly Leu Val Arg Xaa Ala Pro Arg Trp Ile Xaa Gly
                -5                1                5

```

(2) INFORMATION FOR SEQ ID NO: 264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 72..312
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 76..316
id W03477
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..78
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 7..83
id W03477
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 72..328

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 69..325
id W40364
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 3..78
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..76
id W40364
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 164..328
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 172..336
id R71313
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 72..158
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 80..166
id R71313
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 7..78
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 16..87
id R71313
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 164..328
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 151..315
id H87810
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 72..158
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 59..145
id H87810
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 14..78
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 2..66
id H87810
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 72..274
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 52..254
id AA135694
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 20..78
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 1..59
id AA135694
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 270..328
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 249..307
id AA135694
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 62..295
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.9
seq VGAVFGLTTCISA/HV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

```
AGGCTGCCCT TCGCTTCCC GAGCTGGCGG GGTCCGTGGT GCGGGATCGA GATTGCGGGC   60
T ATG GCG CCG AAG GTT TTT CGT CAG TAC TGG GAT ATC CCC GAT GGC ACC   109
  Met Ala Pro Lys Val Phe Arg Gln Tyr Trp Asp Ile Pro Asp Gly Thr
    -75                      -70                      -65

GAT TGC CAC CGC AAA GCC TAC AGC ACC ACC AGT ATT GCC AGC GTC GCT   157
Asp Cys His Arg Lys Ala Tyr Ser Thr Thr Ser Ile Ala Ser Val Ala
  -60                      -55                      -50

GGC CTG ACC GCC GCT GCC TAC AGA GTC ACA CTC AAT CCT CCG GGC ACC   205
Gly Leu Thr Ala Ala Ala Tyr Arg Val Thr Leu Asn Pro Pro Gly Thr
  -45                      -40                      -35

TTC CTT GAA GGA GTG GCT AAG GTT GGA CAA TAC ACG TTC ACT GCA GCT   253
Phe Leu Glu Gly Val Ala Lys Val Gly Gln Tyr Thr Phe Thr Ala Ala
```

-30	-25	-20	-15	
GCT GTC GGG GCC GTG TTT GGC CTC ACC ACC TGC ATC AGC GCC CAT GTC				301
Ala Val Gly Ala Val Phe Gly Leu Thr Thr Cys Ile Ser Ala His Val				
	-10	-5	1	
CGC GAG AAG CCC GAC GAC CCC CTG AAC CGG				331
Arg Glu Lys Pro Asp Asp Pro Leu Asn Arg				
	5	10		

(2) INFORMATION FOR SEQ ID NO: 265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(44..183)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..140
id N78549
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..34)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 150..182
id N78549
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(103..214)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 100..211
id N27605
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 150..203
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq WLQVLPVILLLLG/VP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

```
AGAGAGAGGG GCCGCTACGC CGCACAGCAA ACAAGCTCCG CGACGTTTCC AGGACCCGGA    60
TAATCCCGCC CTTAGAGCAG AGCCGGAAGA AGGCGGGACG AACCGGAAGA GGGTGAAATG   120
CTTTCGGTAG GCACTCCACG GCTGTGAAG ATG GCG GCG GCT GCG TGG CTT CAG     173
                               Met Ala Ala Ala Ala Trp Leu Gln
                               -15

GTG TTG CCT GTC ATT CTT CTG CTT CTG GGA GTC CCC CCG TCG             215
Val Leu Pro Val Ile Leu Leu Leu Leu Gly Val Pro Pro Ser
-10                               -5                               1
```

(2) INFORMATION FOR SEQ ID NO: 266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..124)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 59..182
id AA045287
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..124)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 45..168
id R77973
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..124)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 70..193
id AA136043
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..124)
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 60..183
id AA115201
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(1..124)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 60..183
id R72616
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 5..115
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.8
seq LLILDMNVLYTDA/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

ATAG ATG GAA ATA TAC TTT ATA TTT TGT ATC ATC GTG CCT ATA GCC GCT	49
Met Glu Ile Tyr Phe Ile Phe Cys Ile Ile Val Pro Ile Ala Ala	
-35 -30 -25	
GCC ACC GTG TAT AAA TCC TGG TGT CTG CTC CTT ATC CTG GAC ATG AAT	97
Ala Thr Val Tyr Lys Ser Trp Cys Leu Leu Leu Ile Leu Asp Met Asn	
-20 -15 -10	
GTA TTG TAC ACT GAC GCG TCC CCA CTC GGG	127
Val Leu Tyr Thr Asp Ala Ser Pro Leu Gly	
-5 1	

(2) INFORMATION FOR SEQ ID NO: 267:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 220 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 48..140
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 36..128
id AA054941
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 130..197
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 117..184
id AA054941
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 48..218
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 36..206
id W68324
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 48..141
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 22..115
id H72703
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 130..218
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 103..191
id H72703
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 29..59
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 4..34
id H72703
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 48..140
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 16..108
id AA128297
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 130..218
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 97..185
id AA128297

est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 48..141
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 91
 region 13..106
 id W25240
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 130..218
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 93
 region 94..182
 id W25240
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 71..163
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.8
 seq VLLAIGMFFTAWF/FV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

```

ACTGTCGACG TGTTCTTCCG GTGGCGGACG GCGGATTAGC CTTCGCGGGG CAAAATTGRA      60
RCYCDRGGCC ATG AGC AGA TAT ACC AGC CCA GTG AAC CCA GCT GTC TTC      109
      Met Ser Arg Tyr Thr Ser Pro Val Asn Pro Ala Val Phe
            -30                      -25                      -20

CCC CAT CTG ACC GTG GTG CTT TTG GCC ATT GGC ATG TTC TTC ACC GCC      157
Pro His Leu Thr Val Val Leu Leu Ala Ile Gly Met Phe Phe Thr Ala
            -15                      -10                      -5

TGG TTC TTC GTT TAC GAG GTC ACC TCT ACC AAG TAC ACT CGT GAT ATC      205
Trp Phe Phe Val Tyr Glu Val Thr Ser Thr Lys Tyr Thr Arg Asp Ile
            1                      5                      10

TAT AAA GAG CTC CAG                                          220
Tyr Lys Glu Leu Gln
      15

```

(2) INFORMATION FOR SEQ ID NO: 268:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 422 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 135..179
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 15..59
id R68571
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 309..413
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.8
seq LMLSSSLPLLIWL/KD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

```
AACTTTAGCC TCTGATTGCA GGCCACCACT TCATTACAT GGGGTGAGCA CCAATGCGTT    60
TTGTTCAATT CTTTGTCAA AACCCCAAGA ATCTGGACAA CTTGCACTCA AGACCCTCTA   120
CGGGTTTGGC GAGCCAGTCC TTCAGTGGCT GTTTTCTAGT AGCTCCTTGG CAATTGAGGG   180
GAACTGGCTG GGACCACTCT CCAGTGCTGT CTGAAGGCCA AGGAGTGAAC AGGGATGGCT   240
GCCCTGCCTT GAAGAGGGAA GGA CTCTTTT CTATCCTTTC CAGCTATAGT CCCTGATCCC   300
TACATGTG ATG CGG TTG GCA GCG GAA GCT CAT CCT GGG CGA ACT CAC ACA   350
      Met Arg Leu Ala Ala Glu Ala His Pro Gly Arg Thr His Thr
      -35                -30                -25

CTT TTC AGG AGA CTT AAA CCT TTT CTT ATG CTA AGT TCT TCC CTT CCC   398
Leu Phe Arg Arg Leu Lys Pro Phe Leu Met Leu Ser Ser Ser Leu Pro
      -20                -15                -10

CTA CTC ATC TGG CTA AAG GAC AGA                                422
Leu Leu Ile Trp Leu Lys Asp Arg
      -5                1
```

(2) INFORMATION FOR SEQ ID NO: 269:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 261 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Prostate

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 2..261
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 17..276
id N23506
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 2..220
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 8..226
id R74310
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 219..261
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 226..268
id R74310
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 103..261
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 125..283
id N42319
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 103..261
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 119..277
id N33735
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 105..261
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 143..299
id R23867
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 97..213
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.8
seq IILFSAIVGFIYG/YV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

```

AAGTGCCRRA CCTTAGCCCT CACGGTCCTT AAGTCTCGGT CGCCCTCGCC TCKCAGCCTG   60
CCVBCCGCGC TCRKCTGSSC GACTCCTCAG SCAGCC ATG CTG GAG CAT CTG RGC   114
                               Met Leu Glu His Leu Xaa
                               -35
TCG CTG CCC ACG CAG ATG GAT TAC AAG GGC CAG AAG CTA GCT GRR CAG   162
Ser Leu Pro Thr Gln Met Asp Tyr Lys Gly Gln Lys Leu Ala Xaa Gln
          -30                -25                -20
ATG TTT CAG GGR ATT ATT CTT TTT TCT GCA ATA GTT GGA TTT ATC TAC   210
Met Phe Gln Gly Ile Ile Leu Phe Ser Ala Ile Val Gly Phe Ile Tyr
          -15                -10                -5
GGG TAC GTG GCT GAA CAG TTC GGG TGG ACT GTC TAT ATA GTT ATG GCC   258
Gly Tyr Val Ala Glu Gln Phe Gly Trp Thr Val Tyr Ile Val Met Ala
      1                5                10                15
GGA
Gly
                                           261

```

(2) INFORMATION FOR SEQ ID NO: 270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(154..354)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 70..270
id AA164185
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 28..111
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 298..381
id AA164184
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 297..344
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.8
seq SKVLFCSFSNVLG/FD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

```
CCAACGTGTG CTTTGAAAAA AAGAAGGGAT GTTTCTGTG TCAAATGAAG GTAATCATAG   60
ATCAAATTTG CTTATTGTCT TGTTCAAATC CTAGAAAACC ATTAGCATTT TTCTTTGCTT  120
GTAATATKAG AATCTAACAC TCATACAGAA TATTGGAAAG GTTACCCTAC AATTGTAAAT  180
TTGAAATTCT CCTTCTAATT CTGTCAGTTA TTTATTGACA TAGTAGTGGT TCTGTAGTCA  240
AGTGCATATA AGGTTTGTAA TGTTACATCT TATTNNGGA TTWTTATTTT ATCATT  ATG  299
                                     Met
GAG TAT AGC AAA GTT CTA TTT TGT TCT TTT TCA AAT GTA CTT GGT TTT   347
Glu Tyr Ser Lys Val Leu Phe Cys Ser Phe Ser Asn Val Leu Gly Phe
-15                -10                -5                1

GAT TAT                                     353
Asp Tyr
```

(2) INFORMATION FOR SEQ ID NO: 271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..133
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..115
id HSC13B041
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 124..226
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 105..207
id HSC13B041
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 124..226

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 71..173
id T08849
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 53..133
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..81
id T08849
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 53..135
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..83
id H88132
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 124..192
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 71..139
id H88132
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 192..226
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 140..174
id H88132
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 53..144
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..92
id T33149
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 145..226
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 92..173
id T33149
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 52..133
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..82
id AA121114
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 192..226
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 141..175
id AA121114
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 46..123
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.7
seq LIMQLGSVLLTRC/PF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

```
ACTCTCTGAC TGGGGTGAGG CCGCAGCGGA CTGCCCTTTC CCAAG ATG GCG TCG AAG    57
                                   Met Ala Ser Lys
                                   -25

ATA GGT TCG AGA CGG TGG ATG TTG CAG CTG ATC ATG CAG TTG GGT TCG    105
Ile Gly Ser Arg Arg Trp Met Leu Gln Leu Ile Met Gln Leu Gly Ser
   -20                      -15                      -10

GTG CTG CTC ACA CGC TGC CCC TTT TGG GGC TGC TTC AGC CAG CTC ATG    153
Val Leu Leu Thr Arg Cys Pro Phe Trp Gly Cys Phe Ser Gln Leu Met
   -5                      1                      5                      10

CTG TAC GCT GAG AGG GCT GAG GCA CGC CGG AAG CCC GAC ATC CCA GTG    201
Leu Tyr Ala Glu Arg Ala Glu Ala Arg Arg Lys Pro Asp Ile Pro Val
           15                      20                      25

CCT TAC CTG TAT TTC GAC AGT GGG                                225
Pro Tyr Leu Tyr Phe Asp Ser Gly
           30
```

(2) INFORMATION FOR SEQ ID NO: 272:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 305 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 2..287
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 9..294
id W52125
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 19..283
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..265
id AA024623
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 22..284
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..263
id H55824
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 21..307
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 2..288
id R62921
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 102..287
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 57..242
id N31702
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 45..100
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..56
id N31702
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 69..224
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.7

seq LGLALGRLEGGSA/RH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

```

ATTGGCTCCG GATCGTGCGT GAGGCGGCTT CGTGGGCAGC GAGAGTCACA GACAAGACAG   60
CAAGCAGG ATG GAG CAC TAC CGG AAA GCT GGC TCT GTA GAG CTC CCA GCG   110
      Met Glu His Tyr Arg Lys Ala Gly Ser Val Glu Leu Pro Ala
            -50                      -45                      -40
CCT TCC CCA ATG CCC CAG CTA CCT CCT GAT ACC CTT GAG ATG CGG GTC   158
Pro Ser Pro Met Pro Gln Leu Pro Pro Asp Thr Leu Glu Met Arg Val
            -35                      -30                      -25
CGA GAT GGC AGC AAA ATT CGC AAC CTG CTG GGG TTG GCT CTG GGT CGG   206
Arg Asp Gly Ser Lys Ile Arg Asn Leu Leu Gly Leu Ala Leu Gly Arg
            -20                      -15                      -10
TTG GAG GGC GGC AGT GCT CGG CAT GTA GTG TTC TCA GGT TCT GGC AGG   254
Leu Glu Gly Gly Ser Ala Arg His Val Val Phe Ser Gly Ser Gly Arg
            -5                      1                      5                      10
GCT GCA GGA AAG GCT GTC AGC TGC GCT GAG ATT GTC AAG CGG CGG GTC   302
Ala Ala Gly Lys Ala Val Ser Cys Ala Glu Ile Val Lys Arg Arg Val
            15                      20                      25
CCG
Pro

```

(2) INFORMATION FOR SEQ ID NO: 273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 113..324
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 2..213
id W26501
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 111..324
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 6..219

id W28013
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(211..324)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 334..447
id W28077
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 215..324
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..110
id HSC3LG011
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 104..181
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.6
seq LIALTCLDGTTS/AE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

```

AGCATTTTGC AAAGATGGCT GTAGGAATGG AGGAGCCTGT ATTGCCGCTA ATGTGTGTGC      60
CTGCCCACAA GGCTTCACTG GACCCAGCTG TGAAACGACA TTG ATG AAT GCT CTG      115
                               Met Asn Ala Leu
                               -25

ATG GTT TTG TTC AAT GTG ACA GTC GTG CTA ATT GCA TTA ACC TGC CTG      163
Met Val Leu Phe Asn Val Thr Val Val Leu Ile Ala Leu Thr Cys Leu
   -20                -15                -10

GAT GGT AEC ACT GTG AGT GCA GAG ATG GCT ACC ATG ACA ATG GGA TGT      211
Asp Gly Thr Thr Val Ser Ala Glu Met Ala Thr Met Thr Met Gly Cys
   -5                1                5                10

TTT CAC CAA GTG GAG AAT CGT GTG AAG ATA TTG ATG AGT GTG GGA CCG      259
Phe His Gln Val Glu Asn Arg Val Lys Ile Leu Met Ser Val Gly Pro
          15                20                25

GGA GGC ACA GCT GTG CCA ATG ATA CCA TTT GCT TCA ATT TGG ATG GCG      307
Gly Gly Thr Ala Val Pro Met Ile Pro Phe Ala Ser Ile Trp Met Ala
          30                35                40

GAT ATG ATT GNC GAT                                          322
Asp Met Ile Xaa Asp
          45

```

(2) INFORMATION FOR SEQ ID NO: 274:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 337 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Hypertrophic prostate
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 94..339
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 62..307
 id AA133635
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 32..97
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 1..66
 id AA133635
 est
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 191..325
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.6
 seq VLVYLVTAERVWS/DD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

```

ACTCCCAGGC TGGGCCAGCA CACCCGGCAG GCTCTGTCCT GGAAACAGGC TTCAACGGGC   60
TTCCCCGAAA ACCTTCCCCG CTTCTGGRTA TGAAVWTKCA AGCTGCTTGC TGAGTCCTAT  120
TGCCGGCTGC TGGGAGCMAG GAGAGCCCTG AGGAGTAGTC ACTCAGTAGC AGCTGACGCG  180
TGGGTCCACC ATG AAC TGG AGT ATC TTT GAG GGA CTC CTG AGT GGG GTC   229
      Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val
      -45                -40                -35

AAC AAG TAC TCC ACA GCC TTT GGG CGC ATC TGG CTG TCT CTG GTC TTC   277
Asn Lys Tyr Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe
      -30                -25                -20

ATC TTC CGC GTG CTG GTG TAC CTG GTG ACG GCC GAG CGT GTG TGG AGT   325
Ile Phe Arg Val Leu Val Tyr Leu Val Thr Ala Glu Arg Val Trp Ser
      -15                -10                -5

GAT GAC CAC AAG   337
Asp Asp His Lys
1

```

(2) INFORMATION FOR SEQ ID NO: 275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 205..287
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 37..119
id T82645
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 129..176
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5
seq SLFIYIFXTCSNT/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

```

ACTGTCCCAT TCCTCCCCCT ACAACACACA CACCTTTCAG GCAGGGASGN GATGAGCTTC   60
CAGCCCCAAG AGTGGAGGCT GCCACATCCT AACATASGKA KCTATTGRRR AGGAAKSAGT   120
GTGTATCT ATG ATT ATA TCT CTG TTC ATC TAT ATA TTT TTK ACA TGT AGC   170
    Met Ile Ile Ser Leu Phe Ile Tyr Ile Phe Xaa Thr Cys Ser
      -15                      -10                      -5

AAC ACC TCT CCA TCT TAT CAA KGA ACT CAA CTC GGT CTG GGT CTC CCC   218
Asn Thr Ser Pro Ser Tyr Gln Xaa Thr Gln Leu Gly Leu Gly Leu Pro
      1                      5                      10

AGT GCC CAG TGG TGG CCT TTG ACA GGT AGG AGG ATG CAG TGC TGC AGG   266
Ser Ala Gln Trp Trp Pro Leu Thr Gly Arg Arg Met Gln Cys Cys Arg
    15                      20                      25                      30

CTA TTT TGT TTT KTG TTA CAA   287
Leu Phe Cys Phe Xaa Leu Gln
      35

```

(2) INFORMATION FOR SEQ ID NO: 276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..156
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 40..195
id AA227366
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..156
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 4..159
id AA069390
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 9..152
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..144
id AA248850
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..95
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..78
id AA248912
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 88..132
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 70..114
id AA248912
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 61..108
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4

seq LNSLSALAEAVG/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

```

ATGGCTGTCA GAGGTGGGCG GCTTTGACCG AGAGGCTGCT GGAGCTCGTG TTTGGACGCG      60
ATG TTT CGT CTG AAC TCA CTT TCT GCT TTG GCA GAA CTG GCT GTG GGT      108
Met Phe Arg Leu Asn Ser Leu Ser Ala Leu Ala Glu Leu Ala Val Gly
  -15                      -10                      -5

TCT CGA TGG TAC CAT GGA GGA TCA CAG CCC ATC CAG ATC CGG CGG AGA      156
Ser Arg Trp Tyr His Gly Gly Ser Gln Pro Ile Gln Ile Arg Arg Arg
  1                      5                      10                      15

```

(2) INFORMATION FOR SEQ ID NO: 277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 98..330
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 69..301
id R99696
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 29..98
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..70
id R99696
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 206..330
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 164..288
id W90165
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 98..209

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 55..166
id W90165
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 43..98
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 1..56
id W90165
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 98..330
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 82..314
id H91200
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 16..98
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 1..83
id H91200
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 98..249
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 62..213
id R06513
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 238..288
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.4
seq TLRTWLCCAGSWA/VE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

```
ACATACTTGC AGCTARAAC TAAATATTGCT GCTTGGGGAC CTCCTTCTAG CCTTAAATTT    60
CAGCTCATCA CCTTCACCTG CTTGGTCAT GGCTCTGSCT ATTCTCCTTG ATCCTTGCCA    120
TTTGCACCAG ACCTGGATTG CTAGCGTCTC VATCTGGAGT GCGGCTGGTG GGGGGCCTCC    180
ACCGCTGTGA AGGGCGGGTG GAGGTGGAAC AGAAAGGCCA GTGGGGCACC GTGTGTG      237
ATG ACG GCT GGG ACA TTA AGG ACG TGG CTG TGT TGT GCC GGG AGC TGG      285
```

```

Met Thr Ala Gly Thr Leu Arg Thr Trp Leu Cys Cys Ala Gly Ser Trp
   -15                      -10                      -5

GCT GTG GAG CTG CCA GCG GAA CCC CTA GTG GTA TTT TGT AWG AGC ACC    333
Ala Val Glu Leu Pro Ala Glu Pro Leu Val Val Phe Cys Xaa Ser Thr
   1                      5                      10                      15

AGC AGA AAA AGA GCA AAA GGT CTC ATC CAA TCA GTC                    369
Ser Arg Lys Arg Ala Lys Gly Leu Ile Gln Ser Val
          20                      25

```

(2) INFORMATION FOR SEQ ID NO: 278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..99)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 99..196
id AA088690
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(87..187)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 12..112
id AA088690
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 111..182
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3
seq RLLVILCVSVKAG/ST

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

```

ACTACAGCAT GGCCACGTGG AGGCAGCGGC AGGAGAAAAA GCAGCTGGGC TTCTTCTGAA    60
CCCAAGCCCT CTCGACTGCC CCTATCCCCT GGAVCCCCAA CATACCTACA ATG CTG      116
                                     Met Leu
GGG AGG CCC TGC TTC CAC TCC CCT CAG AGG CTT TTG GTC ATC CTC TGC      164

```


Gly Arg Pro Cys Phe His Ser Pro Gln Arg Leu Leu Val Ile Leu Cys
-20 -15 -10

GTG TCA GTA AAA GCA GGC AGC ACG
Val Ser Val Lys Ala Gly Ser Thr
-5 1

188

(2) INFORMATION FOR SEQ ID NO: 279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 106..261
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 119..274
id AA280906
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..99
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 15..112
id AA280906
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 260..291
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 272..303
id AA280906
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 140..291
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 224..375
id HUM406F04B
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 12..112
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 1..101
id HUM406F04B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 106..140
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 94..128
id HUM406F04B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 132..261
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 124..253
id AA133362
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 5..92
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..88
id AA133362
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 260..291
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 251..282
id AA133362
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 106..261
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 94..249
id N57260
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 10..92
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..83
id N57260
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 260..291
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 247..278
 id N57260
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 41..234
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 42..235
 id W25567
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 1..40
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 1..40
 id W25567
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 194..277
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.2
 seq LQFVLPVATQIQQ/EV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

```

AGGGGCGTTG GGAACGGTTG TAGGACGTGG CTCTTTATTC GTGAGTTTTC CATTTACCTC   60
CGTGTAACCT AGAGCTTCAG ACGCCCTATG GCGTCCGCCT CGACACCAAC CGGCGGCCTT  120
GAGCGCTGAG CAAGCAAAGG TGGTCCTCGC GGAGGTGATC CAGGCGTTCT CCGCCCCGGA  180
GAATGCAGTG CGC ATG GAC GAG GCT CGG GAT AAC GCC TGC AAC GAC ATG   229
          Met Asp Glu Ala Arg Asp Asn Ala Cys Asn Asp Met
          -25                               -20

GGT AAG ATG CTG CAA TTC GTG CTG CCC GTG GCC ACG CAG ATC CAG CAG   277
Gly Lys Met Leu Gln Phe Val Leu Pro Val Ala Thr Gln Ile Gln Gln
-15                               -10                               -5

GAG GTT ATC AAA
Glu Val Ile Lys
1

```

(2) INFORMATION FOR SEQ ID NO: 280:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 355 base pairs

- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 38..69
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..32
id H56508
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 287..349
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq LCALGSAPSSMWA/GE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

```

AAACCTCCGT GGCTAGTCTT GACGTGGCGG GTTGCTTTCC AAAATGGCGC GGGTGCTGAA   60
GGCTGCAGCC GCDBAATGCC GTAGGTGAAT ACCGGGCACC GCCGACCTTC GCCATGGGAC  120
AGGGAGCGTG GGAACGGCGG TCGGGGGCGG AGGAKGCCTC GGTGTGGCCA AAGCACCTTG  180
ATCTAATGTC CTCCCCGGG GCGCGTTCC ACAGCAGCTG CTGTCACTTW KGGCAGAGGG  240
TGCCTTCCAG AAGCGCCACC GCTTAGTAGC GGGGATTGCB TTGTGC ATG AGT CCC   295
                               Met Ser Pro
                               -20

ATT TCE ATC CGA GAG CTG TGC GCC TTG GGC TCT GCA CCT TCC AGT ATG   343
Ile Ser Ile Arg Glu Leu Cys Ala Leu Gly Ser Ala Pro Ser Ser Met
      -15                -10                -5

TGG GCB GGA GAG                               355
Trp Ala Gly Glu
      1

```

(2) INFORMATION FOR SEQ ID NO: 281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

GAC CTC TTA AGT GCC TCA CCC TGG GCC CTC ACT ATT GTT TCC AGT GAG	105
Asp Leu Leu Ser Ala Ser Pro Trp Ala Leu Thr Ile Val Ser Ser Glu	
-10 -5 1 5	
CTC CAC CTT GCT CCA TCC ATG ACC ACA GTG GAC CAG CTC GAG TCT CAA	153
Leu His Leu Ala Pro Ser Met Thr Thr Val Asp Gln Leu Glu Ser Gln	
10 15 20	
GTG GAC AAT GTK ATC TTA CAG ACT GGA GAG AGT GCT AGT GAA TGC TTT	201
Val Asp Asn Val Ile Leu Gln Thr Gly Glu Ser Ala Ser Glu Cys Phe	
25 30 35	
TGT CTT CAA TGC CCA TCT CTT GGA AAT ATT GAA GGT GGA GTA GCA ACC	249
Cys Leu Gln Cys Pro Ser Leu Gly Asn Ile Glu Gly Gly Val Ala Thr	
40 45 50	
GGG CAY HGG	258
Gly His Xaa	
55	

(2) INFORMATION FOR SEQ ID NO: 282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 6..202
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 10..206
id AA074428
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 193..254
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 196..257
id AA074428
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 28..202
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..175

id AA158941
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 193..285
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 165..257
id AA158941
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 37..202
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..166
id AA148039
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 193..254
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 156..217
id AA148039
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 250..285
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 214..249
id AA148039
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 74..280
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..207
id H72224
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 76..153
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.2
seq LTCGPALVPRLWA/TC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

AAGAGGCTAG AAGCTGGATT CAGCGTGTCC GCGACCTCAC CTTTAGGTCC TGTGAGGGAC 60

GGCCCAGGTG GCAGG ATG TCC TGG TCT GGC CTT CTC CAT GGC CTC AAC ACG 111

	Met Ser Trp Ser Gly Leu Leu His Gly Leu Asn Thr	
	-25 -20 -15	
TCC CTA ACT TGT GGC CCA GCT CTG GTT CCC CGG CTC TGG GCT ACC TGC		159
Ser Leu Thr Cys Gly Pro Ala Leu Val Pro Arg Leu Trp Ala Thr Cys		
	-10 -5 1	
TCC ATG GCT ACC CTG AAC CAG ATG CAC CGC CTG GGG CCC CCC AAG CGG		207
Ser Met Ala Thr Leu Asn Gln Met His Arg Leu Gly Pro Pro Lys Arg		
	5 10 15	
CCG CCT CGG AAG CTG GGC CCC ACG GAA GGC CGG CCG CAG CTG AAG GGT		255
Pro Pro Arg Lys Leu Gly Pro Thr Glu Gly Arg Pro Gln Leu Lys Gly		
	20 25 30	
GTG GTC CTG TGC ACG TTT ACC CGC AAC CGG		285
Val Val Leu Cys Thr Phe Thr Arg Asn Arg		
	35 40	

(2) INFORMATION FOR SEQ ID NO: 283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..223
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 1..206
id HSC3CC061
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 112..223
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 94..205
id H33976
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 49..93
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 1..45
id AA041823
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 49..93
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 93
 region 1..45
 id AA003782
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 25..93
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.1
 seq LEAFSQAISAIQA/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

```

AAKAGCTGCT GTGGCGGCGG CAAC ATG GCG GAC GTG ATA AAT GTC AGT GTG      51
                        Met Ala Asp Val Ile Asn Val Ser Val
                        -20                               -15

AAC CTG GAG GCC TTT TCC CAG GCC ATT AGT GCC ATC CAG GCG CTG CGA      99
Asn Leu Glu Ala Phe Ser Gln Ala Ile Ser Ala Ile Gln Ala Leu Arg
      -10                               -5                               1

TCC AGC GTG AGC AGG GTG TTC GAC TGC CTG AAG GAT GGG ATG CGG AAC      147
Ser Ser Val Ser Arg Val Phe Asp Cys Leu Lys Asp Gly Met Arg Asn
      5                               10                               15

AAG GAG ACG CTG GAG GGC CGG GAG AAG GCC TTT ATT GCG CAC TTC CAG      195
Lys Glu Thr Leu Glu Gly Arg Glu Lys Ala Phe Ile Ala His Phe Gln
      20                               25                               30

GAC AAC TTA CAT TCG GTC AAC CGG GAC CCA                                225
Asp Asn Leu His Ser Val Asn Arg Asp Pro
      35                               40

```

(2) INFORMATION FOR SEQ ID NO: 284:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: complement(210..340)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99

region 172..302
id AA062591
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 109..204
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq RLLSSLLLTMSNN/NP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

```
AGACCCGATG GACCCCGGCG ACGCSCCATT TTGGAGTCTT CCCTAAGGAT CCTCTACCGG      60
CTTTTCGAGT CAGTGCTGCC GCCGCTGCCC GCGGCTTTGC AGAGCAGG ATG AAT GTG      117
                                         Met Asn Val
                                         -30

ATA GAC CAC GTG CGG GAC ATG GCG GCC GCG GGG CTG CAC TCC AAC GTG      165
Ile Asp His Val Arg Asp Met Ala Ala Ala Gly Leu His Ser Asn Val
          -25                      -20                      -15

CGG CTC CTC AGC AGC TTG TTA CTT ACA ATG AGT AAT AAC AAC CCT GAG      213
Arg Leu Leu Ser Ser Leu Leu Leu Thr Met Ser Asn Asn Asn Pro Glu
          -10                      -5                      1

TTA TTC TCC CCA CCT CAG AAG TAC CAG CTT TTG GTG TAT CAT GCA GAT      261
Leu Phe Ser Pro Pro Gln Lys Tyr Gln Leu Leu Val Tyr His Ala Asp
          5                      10                      15

TCT CTC TTT CAT GAT AAG GAA TAT CGG AAT GCT GTG AGT AAG TAT ACC      309
Ser Leu Phe His Asp Lys Glu Tyr Arg Asn Ala Val Ser Lys Tyr Thr
          20                      25                      30                      35

ATG GCT TTA CAG CAG AAG AAA GCG CTA AGT      339
Met Ala Leu Gln Gln Lys Lys Ala Leu Ser
          40                      45
```

(2) INFORMATION FOR SEQ ID NO: 285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..41)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90

region 66..105
id AA085310
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 70..117
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq ACLAWTAVRPSAC/CH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

```
AAAGTGAGTT TGCGAACGGA GCAGCTGCTG CAGCAGGGCC CATGGCGGAC ACCCAGTACA    60
TCCTGCCCCA ATG ACA TCG GCG TGT CTA GCC TGG ACT GCC GTG AGG CCT TCC    111
      Met Thr Ser Ala Cys Leu Ala Trp Thr Ala Val Arg Pro Ser
      -15                -10                -5

GCC TGC TGT CAC CCA CAG AGC GCC AAC TGG                                141
Ala Cys Cys His Pro Gln Ser Ala Asn Trp
      1                5
```

(2) INFORMATION FOR SEQ ID NO: 286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(147..290)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 141..284
id W12393
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 249..289
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..41
id HSC2TF111
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 60..224

(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4
seq VFGMSSSSGASNS/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

```
ATCTCAACTT GGACTTGCAA TCACAGAACA TTTACCACCA TGGAAGAGAA GGAAGTAGG      59

ATG AAT GGA AGT AGG ACT CTA ACG CAC AGC ATT AGT GAT GGA CAA CTT      107
Met Asn Gly Ser Arg Thr Leu Thr His Ser Ile Ser Asp Gly Gln Leu
-55                -50                -45                -40

CAA GGT GGC CAG TCC AAT AGT GAA CTA TTT CAG CAG GAG SSA CAG ACA      155
Gln Gly Gly Gln Ser Asn Ser Glu Leu Phe Gln Gln Glu Xaa Gln Thr
                -35                -30                -25

GCA CCA GCT CAA GTT CCT CAA GGC TTT AAT GTT TTT GGA ATG TCC AGT      203
Ala Pro Ala Gln Val Pro Gln Gly Phe Asn Val Phe Gly Met Ser Ser
                -20                -15                -10

TCC TCT GGT GCT TCA AAT TCA GCA CCA CAT CTT GGA TTT CAC TTA GGC      251
Ser Ser Gly Ala Ser Asn Ser Ala Pro His Leu Gly Phe His Leu Gly
                -5                1                5

AGC AAA GGA ACA TCT AGC CTT TCT CAA CAA ACT CCC GGG      290
Ser Lys Gly Thr Ser Ser Leu Ser Gln Gln Thr Pro Gly
10                15                20
```

(2) INFORMATION FOR SEQ ID NO: 287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(68..194)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 204..330
id N35493
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(208..323)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 75..190
id N35493

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..79)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 318..395
id N35493
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 186..233
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq FFLFLSFVLMYDG/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

```
ATAAAAGAAG CAGCAAATAG AATTTCCAC AAAGTAAGTT GACTCTAAAT CTTAAGTATT   60
ACCTAGTTTT TTAAAGGTTT GAATATAATA ATGCAGTATT TGCAGTATAA AAAGGAAGGA  120
ATTTGTAGAG AATCATTTTG GTGCTCAAGT CTCTTAGCAG TGCCTTATTG CCTCATAGCA  180
AGAAG ATG CTG GGG TTT TTT TTG TTT TTG TCC TTT GTA TTA ATG TAT GAT   230
Met Leu Gly Phe Phe Leu Phe Leu Ser Phe Val Leu Met Tyr Asp
      -15                      -10                      -5

GGT TTG CGC CTT TTT GGC ATT CTT TCA ACA TGT CGT GTA CAT CAC ACC   278
Gly Leu Arg Leu Phe Gly Ile Leu Ser Thr Cys Arg Val His His Thr
      1                      5                      10                      15

ATG AAT CAG TTC CTA ATT GAT ATA TCT AGC TTT ACC TCC CGA GTT CGG   326
Met Asn Gln Phe Leu Ile Asp Ile Ser Ser Phe Thr Ser Arg Val Arg
      20                      25                      30
```

(2) INFORMATION FOR SEQ ID NO: 288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 219..380
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 46..207

id N95583
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 219..335
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 46..162
id AA283710
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 336..380
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 162..206
id AA283710
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 240..320
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4
seq SIKVLLQSALSLG/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

```

AGTGGCTCTT CTGACCCAAG GCCCCGCCGT CCAGGTAGGG GGCTGTGGCC TCTAGGGATC   60
AGGGACTACT TACCTGCGAA TCCCGGTTGC CCGCCCGCCA RCACGTCCGK TYCCSTAARG   120
CARAMCGCCT KGGCTCCTGG CTGAACCGTC TTCTCAMCGT TTGSCGGAGT CTGAMCTCCC   180
CACGCTTAGT CCACTAACGR AGCTATCCCT GCTCCTGMCC CACAGCTTCT AAGTGCCAG   239
ATG ATG GAG GAG CGT GCC AAC CTG ATG CAC ATG ATG AAA CTC AGC ATC   287
Met Met Glu Glu Arg Ala Asn Leu Met His Met Met Lys Leu Ser Ile
- 25                      -20                      -15

AAG GTG TTG CTC CAG TCG GCT CTG AGC CTG GGC CGC AGC CTG GAT GCG   335
Lys Val Leu Leu Gln Ser Ala Leu Ser Leu Gly Arg Ser Leu Asp Ala
-10                      -5                      1                      5

GAC CAT GCC CCC TTG CAG CAG TTC TTT GTA GTG ATG GAG CAC TGC TCA   383
Asp His Ala Pro Leu Gln Gln Phe Phe Val Val Met Glu His Cys Ser
10                      15                      20

```

(2) INFORMATION FOR SEQ ID NO: 289:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 319 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 57..180

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97
region 15..138
id AA090170
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 226..286

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98
region 184..244
id AA090170
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 21..242

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 90
region 1..222
id HSU46267
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 143..319

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 90
region 220..396
id AA048294
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 149..286

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 92
region 139..276
id AA118611
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 143..286

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 92
region 88..231
id AA063937
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 80..130
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.9
 seq XIVSAALLAFVQT/HL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

```

AGTTGGTGGG GCTGGGGGAT GAGAGCTGCA CCGCGCGGGA YAAGTCGCCG GCGGCGCCCC 60
AMGGAGCAGA ACAGAGAGC ATG GAG CTG GAG AKG ATC GTC AGT GCA GCC CTC 112
      Met Glu Leu Glu Xaa Ile Val Ser Ala Ala Leu
      -15                               -10

CTT GCC TTT GTC CAG ACA CAC CTC CCG GAG GCC GAC CTC AGT GGC TTG 160
Leu Ala Phe Val Gln Thr His Leu Pro Glu Ala Asp Leu Ser Gly Leu
      -5                               1                               5                               10

GAT GAG GTC ATC TTC TCC TAT GTG CKT GGG GTC CTG GAG GAC CTG GGC 208
Asp Glu Val Ile Phe Ser Tyr Val Xaa Gly Val Leu Glu Asp Leu Gly
      15                               20                               25

CCC TCG GGC CCA TCA GAG GAG AAC TTC GAT ATG GAG GCT TTC ACT GAG 256
Pro Ser Gly Pro Ser Glu Glu Asn Phe Asp Met Glu Ala Phe Thr Glu
      30                               35                               40

ATG ATG GAG GCC TAK GTG CCT GGC TTC GCC CAC ATC CCC AGG GGM ACA 304
Met Met Glu Ala Xaa Val Pro Gly Phe Ala His Ile Pro Arg Gly Thr
      45                               50                               55

ATA GGG GAS ATG ATG 319
Ile Gly Xaa Met Met
      60
  
```

(2) INFORMATION FOR SEQ ID NO: 290:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 274 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 2..273
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 93
 region 8..279
 id T30552
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 3..273
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 92
 region 1..271
 id C14403
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 2..273
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 92
 region 14..285
 id T30625
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 4..273
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 92
 region 1..270
 id T32136
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 3..270
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 93
 region 1..268
 id C14440
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 98..175
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.9
 seq SLIPLFXFIGTGA/TG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

```

AGGAAGTCCG TAGTGTCTCA TTGCRGATAA TTTTAGCTT AGGGCCTKGT GGCTAGGKCG      60
GTTCTCTCCK KTCCAGTCGG AGACCTCTGC SGVRRRC ATG CTC CGC CAG ATC ATC      115
                Met Leu Arg Gln Ile Ile
                -25

GGT CAG GCC AAG AAG CAT CCG AGC TTG ATC CCC CTC TTT KTA TTT ATT      163
Gly Gln Ala Lys Lys His Pro Ser Leu Ile Pro Leu Phe Xaa Phe Ile
-20                -15                -10                -5

GGR ACT GGA GCT ACT GGA GCA ACA CTG TAT CTC TTG CGT CTG GCA TTG      211
Gly Thr Gly Ala Thr Gly Ala Thr Leu Tyr Leu Leu Arg Leu Ala Leu
                1                5                10

TTC AAT CCA GRT GTT TGT TGG GAC AGA RRT AAC CCA GAG CCC TGG AAC      259
Phe Asn Pro Xaa Val Cys Trp Asp Arg Xaa Asn Pro Glu Pro Trp Asn

```


15

20

25

RRA CTG GGC CCC GAA
Xaa Leu Gly Pro Glu
30

274

(2) INFORMATION FOR SEQ ID NO: 291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 200..332
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 5..137
id T78510
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(230..332)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 117..219
id R46866
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 37..330
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq WTSLTCSLVVVDG/CG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

AAGTGC	GGTG	GAGCC	AGGCG	TGGA	AGTC	GACACA	AGATG	GTGAAG	GAGACC	CAG	54					
							Met	Val	Lys	Glu	Thr	Gln				
												-95				
TAC	TAT	GAC	ATC	CTG	GGC	GTG	AAG	CCC	AGC	GCG	TCC	CCG	GAG	AGA	TCA	102
Tyr	Tyr	Asp	Ile	Leu	Gly	Val	Lys	Pro	Ser	Ala	Ser	Pro	Glu	Arg	Ser	
		-90					-85					-80				
AGA	AGG	CCT	ATC	GGA	AGC	TGG	CGC	TCA	AGT	ACC	ACC	CGG	ACA	AGA	ACC	150
Arg	Arg	Pro	Ile	Gly	Ser	Trp	Arg	Ser	Ser	Thr	Thr	Arg	Thr	Arg	Thr	
		-75					-70					-65				

CGG	ATG	AGG	GCG	AGA	AGT	TTA	AAC	TCA	TAT	CCC	AGG	CAT	ATG	AAG	TGC	198
Arg	Met	Arg	Ala	Arg	Ser	Leu	Asn	Ser	Tyr	Pro	Arg	His	Met	Lys	Cys	
-60					-55					-50					-45	
TTT	CAG	ATC	CAA	AGA	AAA	GGG	ATG	TTT	ATG	ACC	AAG	GCG	GAG	AGC	AGG	246
Phe	Gln	Ile	Gln	Arg	Lys	Gly	Met	Phe	Met	Thr	Lys	Ala	Glu	Ser	Arg	
				-40					-35					-30		
CAA	TBV	AAG	AAG	GAG	GCT	CAG	GCA	GCC	CCA	GCT	TCT	CTT	CAC	CCA	TGG	294
Gln	Xaa	Lys	Lys	Glu	Ala	Gln	Ala	Ala	Pro	Ala	Ser	Leu	His	Pro	Trp	
			-25					-20					-15			
ACA	TCT	TTG	ACA	TGT	TCT	TTG	GTG	GTG	GTG	GAC	GGA	TGC	GGG			336
Thr	Ser	Leu	Thr	Cys	Ser	Leu	Val	Val	Val	Asp	Gly	Cys	Gly			
		-10					-5					1				

(2) INFORMATION FOR SEQ ID NO: 292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- [illegible]

(ix) FEATURE:

- [illegible]

(ix) FEATURE:

- (A) NAME/KEY: other
(B) LOCATION: 359..396
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
 region 347..384
 id W25476
 est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 21..278
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 19..276
id HUM179H07B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 279..379
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 278..378
id HUM179H07B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 17..175
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 27..185
id AA002128
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 171..292
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 182..303
id AA002128
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 358..396
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 373..411
id AA002128
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 325..358
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 339..372
id AA002128
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 204..396
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 186..378
id AA253291
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 22..202
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 5..185
 id AA253291
 est

(ix) FEATURE:

[illegible]

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 251..359
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 234..342
id W45609
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 363..396
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 348..381
id W45609
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 59..166
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.8
seq RALSTXLFGSIRG/AA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

AGTGC GCAG GGC GCCGATC ACCACAAC																58		
ATG	GCA	AAT	CTT	TTT	ATA	AGG	AAA	ATG	GTG	AAC	CCT	CTG	CTC	TAT	CTC	106		
Met	Ala	Asn	Leu	Phe	Ile	Arg	Lys	Met	Val	Asn	Pro	Leu	Leu	Tyr	Leu			
				-35					-30					-25				
AGT CGT CAC ACG GTG AAG CCT CGA GCC CTC TCC ACA NTT CTA TTT GGA																154		
Ser	Arg	His	Thr	Val	Lys	Pro	Arg	Ala	Leu	Ser	Thr	Xaa	Leu	Phe	Gly			
				-20					-15					-10				-5
TCC ATT CGA GGT GCA GCC CCC GTG GCT GTG GAA CCC GGG GCA GCA GTG																202		
Ser	Ile	Arg	Gly	Ala	Ala	Pro	Val	Ala	Val	Glu	Pro	Gly	Ala	Ala	Val			
				1					5					10				

CGC TCA CTT CTC TCA ³ CCC GGC CTC CTG CCC CAT CTG CTG CCT GCG CTG	250
Arg Ser Leu Leu Ser Pro Gly Leu Leu Pro His Leu Leu Pro Ala Leu	
15 20 25	
GGG TTC AAA AAC AAG ACT GTC CTT AAG AAG CGC TGC AAG GAC TGT TAC	298
Gly Phe Lys Asn Lys Thr Val Leu Lys Lys Arg Cys Lys Asp Cys Tyr	
30 35 40	
CTG GTG AAG AGG CGG GGT CGG TGG TAC GTC TAC TGT AAA ACC CAT CCG	346
Leu Val Lys Arg Arg Gly Arg Trp Tyr Val Tyr Cys Lys Thr His Pro	
45 50 55 60	
AGG CAC AAG CAG AGA CAC ATG TAN ACC CTT TCC CTC CAG AGT CAC GCA	394
Arg His Lys Gln Arg His Met Xaa Thr Leu Ser Leu Gln Ser His Ala	
65 70 75	
CAA	397
Gln	

(2) INFORMATION FOR SEQ ID NO: 293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 115..216
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 41..142
id H64274
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 74..116
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..43
id H64274
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 115..216
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 36..137
id R16956
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 79..116
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..38
id R16956
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 123..214
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 57..148
id W04201
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 71..124
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 4..57
id W04201
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 123..190
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 50..117
id N76590
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 75..116
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 2..43
id N76590
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(107..195)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 323..411
id N70265
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 106..201
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7
seq RIHLCQRSPGSQG/VR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

```

ACCCTGCCTC ATGCAGCCTA TGGGCTAGGC TTTAGGGTCC GCGGTTGGTC AKACCGGAGC   60
ACTTGGCCTG AAGACCTGGA ATTGGYGACT TCGATATTAA CAAGG ATG GCG GCG GCC   117
                                     Met Ala Ala Ala
                                     -30

GCA GCA AGT CGA GGA KTC GGG GCA AAG CTG GGC CTG CGT GAN ATT CGC   165
Ala Ala Ser Arg Gly Xaa Gly Ala Lys Leu Gly Leu Arg Xaa Ile Arg
                -25                -20                -15

ATC CAC TTA TGT CAG CGC TCG CCC GGC AGC CAG GGC GTC AGG GAC TTC   213
Ile His Leu Cys Gln Arg Ser Pro Gly Ser Gln Gly Val Arg Asp Phe
                -10                -5                1

ATT
Ile
5
216

```

(2) INFORMATION FOR SEQ ID NO: 294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..279)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..279
id M85423
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(196..289)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 466..559
id AA126476
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(133..194)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 560..621
id AA126476
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(105..137)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 616..648
id AA126476
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 152..292
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..141
id R33928
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 160..292
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 14..146
id H67425
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 161..292
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..132
id W04820
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 101..232
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq IALTLIPSMLSRA/AG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

```
AACTTCTTCA TCTTGGTGGT CCTGCCCAG TTATTTTGCC TCATTAGACA TCAAGAAATG   60
GAGAAAGACT GAAAGTTAAT ATCTTAAGTG CTTGTTCTTC ATG TTT CCT TCT TGT   115
                               Met Phe Pro Ser Cys
                               -40
TAT TTA TGC TAT TCT CTT TGT GGC TCC ATT CTT CTT TCA ATC TTC TCA   163
Tyr Leu Cys Tyr Ser Leu Cys Gly Ser Ile Leu Leu Ser Ile Phe Ser
-35 -30 -25
GCT TAT AAC CGT CTT TCC CTT ATG CTA AGG ATA GCC CTT ACA CTC ATC   211
```


Ala Tyr Asn Arg Leu Ser Leu Met Leu Arg Ile Ala Leu Thr Leu Ile
-20 -15 -10

CCA TCT ATG CTG TCA AGG GCT GCT GGT TGG TGC TGG TAC AAG GAG CCC 259
Pro Ser Met Leu Ser Arg Ala Ala Gly Trp Cys Trp Tyr Lys Glu Pro
-5 1 5

ACT CAG CAG TTT TCT TAC CTT TGC CTG CCC TGC GGG 295
Thr Gln Gln Phe Ser Tyr Leu Cys Leu Pro Cys Gly
10 15 20

(2) INFORMATION FOR SEQ ID NO: 295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(9..318)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 36..345
id R32875
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(52..318)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 35..301
id N69845
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(9..52)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 302..345
id N69845
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(39..318)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 46..325
id H20723

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(30..318)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 35..323
id HSC3JH072
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(65..318)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 43..296
id R02144
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 125..304
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7
seq QLXFLYFVCCIFQ/DV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

```

AAMAAGCTCC CAGCCTCCAG AGGCTCTCAA TGAAGAGTCA CCTTCATGGT CGTCTYCAGG    60
AACAGGACGG ATGAMGAAGG GGTGGGGTTA AGACTCAGGG GCACCTGAGG GTCTGAGCCC    120
CCTT ATG AGT ACC CAA GAM GGA CTG TCT ATG CAT GCA CAC CCA CAA GCC    169
  Met Ser Thr Gln Xaa Gly Leu Ser Met His Ala His Pro Gln Ala
   -60                      -55                      -50

TAT ACA CCA TTT ATA TAC CTA CAC GCA CGC AAG AGA CGC GGA GAG ATA    217
Tyr Thr Pro Phe Ile Tyr Leu His Ala Arg Lys Arg Arg Gly Glu Ile
   -45                      -40                      -35                      -30

GGC GAT GCA GAC TCG CGA TTC AAT GAT CGA TAT GCT CAT AAR AGT GCT    265
Gly Asp Ala Asp Ser Arg Phe Asn Asp Arg Tyr Ala His Lys Ser Ala
                   -25                      -20                      -15

CAA TTA TMT TTT CTG TAT TTT GTA TGC TGT ATT TTC CAA GAC GTA TAT    313
Gln Leu Xaa Phe Leu Tyr Phe Val Cys Cys Ile Phe Gln Asp Val Tyr
                   -10                      -5                      1

TAT KTN    319
Tyr Xaa
  5

```

(2) INFORMATION FOR SEQ ID NO: 296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Prostate

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(1..170)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 118..287
id AA035134
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(1..170)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 116..285
id N54275
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(1..170)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 119..288
id AA088715
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(19..170)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 115..266
id N78023
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(12..133)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 157..278
id AA100730
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(127..170)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 119..162
id AA100730

est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 56..118
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7
seq SSCSCSLISFTRG/DK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

```

ATCTTAGTGC CTTTATCTGT CTTTATGTCT TGGGGTTGGG GTAGGTAGAT ACCAA ATG      58
                                         Met
AAA CAC TTT CAG GAC CTT CCT TCC TCT TGC AGT TGT TCT TTA ATC TCC      106
Lys His Phe Gln Asp Leu Pro Ser Ser Cys Ser Cys Ser Leu Ile Ser
-20                               -15                -10                -5

TTT ACT AGA GGA GAT AAA TAT TTT GCA TAT AAT GAA GAA ATT TTT CTA      154
Phe Thr Arg Gly Asp Lys Tyr Phe Ala Tyr Asn Glu Glu Ile Phe Leu
                               1                   5                   10

GTA TAT AAC GCA GAC CAG                                              172
Val Tyr Asn Ala Asp Gln
                        15

```

(2) INFORMATION FOR SEQ ID NO: 297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(29..369)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 103..443
id W26961
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(383..424)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 48..89
id W26961
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(34..369)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 100..435
id W26018
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(383..424)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 45..86
id W26018
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(200..369)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 111..280
id W26871
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(143..200)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 281..338
id W26871
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(383..424)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 56..97
id W26871
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(94..123)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 361..390
id W26871
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(119..369)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 104..354
id W26098

est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: complement(383..424)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 49..90
 id W26098
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 31..302
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 1..272
 id N99777
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 302..369
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 273..340
 id N99777
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 155..340
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.7
 seq SILGIISVPLSIG/YC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

```

AGTGAAAAGA AGATGCCTAG AGAATGGCAA TTAAAAGAA AAAGATATAC TTGTTTGGCC      60
CCTTGAECTG ACCGACACTG GTTCCCATGA AGCGGCTACC AAAGCTGTTT TCCAGGAGTT      120
TGGTAGAATC GACATTCTGG TCAACAATGG TGGA ATG TCC CAG CGT TCT CTG TGC      175
                               Met Ser Gln Arg Ser Leu Cys
                               -60

ATG GAT ACC AGC TTG GAT GTC TAC AGA RAG CTA ATA GAG CTT AAC TAC      223
Met Asp Thr Ser Leu Asp Val Tyr Arg Xaa Leu Ile Glu Leu Asn Tyr
-55                      -50                      -45                      -40

TTA GGG ACG GTG TCC TTG ACA AAA TGT GTT CTG CCT CAC ATG ATC GAG      271
Leu Gly Thr Val Ser Leu Thr Lys Cys Val Leu Pro His Met Ile Glu
                      -35                      -30                      -25

AGG AAG CAN KKA AAG ATT GTT ACT GTG AAT AGC ATC CTG GGT ATC ATA      319
Arg Lys Xaa Xaa Lys Ile Val Thr Val Asn Ser Ile Leu Gly Ile Ile
                      -20                      -15                      -10

TCT GTA CCT CTT TCC ATT GGA TAC TGT GCT AGC RAG CAT GCT CTS HGG      367
Ser Val Pro Leu Ser Ile Gly Tyr Cys Ala Ser Xaa His Ala Leu Xaa

```

-5

1

5

GGT TTT TTT AAT RDH CTT CGA ACA GAD CTT GCC ACA TAC CCA GGT ATA 415
Gly Phe Phe Asn Xaa Leu Arg Thr Xaa Leu Ala Thr Tyr Pro Gly Ile
10 15 20 25
ATA GTT TCT 424
Ile Val Ser

(2) INFORMATION FOR SEQ ID NO: 298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 179..348
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 160..329
id AA159241
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 103..184
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 83..164
id AA159241
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 383..437
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 366..420
id AA159241
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 21..66
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..46
id AA159241
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 342..383
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 324..365
id AA159241
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 66..102
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 47..83
id AA159241
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 103..215
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 81..193
id AA076222
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 216..329
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 195..308
id AA076222
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..102
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..81
id AA076222
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 390..437
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 374..421
id AA076222
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 342..377
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 324..359
id AA076222

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 241..443
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 202..404
id AA149750
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 40..215
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..176
id AA149750
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 241..443
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 181..383
id W63593
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 63..184
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 3..124
id W63593
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 179..243
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 120..184
id W63593
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 320..438
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 267..385
id AA130386
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 216..328
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 164..276
id AA130386
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 103..215
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 50..162
id AA130386
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 82..375
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.6
seq LALRTSWISSVCS/VT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

```

AAGTGACGCG GCCCAAGGGC GGAAGTGAGA AAGTTGTCTG CGTCTCGAGG CGAGTTGGCG      60
GACTGTGCGC GCGGCGGGGC G ATG GGG GGC TCG GGC AGT CGC CTG TCC AAG      111
               Met Gly Gly Ser Gly Ser Arg Leu Ser Lys
               -95                               -90

GAG CTG CTG GCC GAR TAC CAG GAC TTG ACG TTC CTG ACG AAG CAG GAG      159
Glu Leu Leu Ala Glu Tyr Gln Asp Leu Thr Phe Leu Thr Lys Gln Glu
               -85                               -80               -75

ATC CTC CTA GCC CAC AGG CGG TTT TGT GAG CTG CTT CCC CAG GAG CAG      207
Ile Leu Leu Ala His Arg Arg Phe Cys Glu Leu Leu Pro Gln Glu Gln
               -70                               -65               -60

CGG ASK NGG AGT CGT CAC TTC GGG CAC AAG TGC CCT TCG AGC AGA TTC      255
Arg Xaa Xaa Ser Arg His Phe Gly His Lys Cys Pro Ser Ser Arg Phe
               -55                               -50               -45

TCA GCE TTC CAG AGC TCA AGG CCA ACC CCT TCA AGG AGC GAA TCT GCA      303
Ser Ala Phe Gln Ser Ser Arg Pro Thr Pro Ser Arg Ser Glu Ser Ala
               -40                               -35               -30               -25

GGG TCT TCT CCA CAT CCC CAG CCA AAG ACA GCC TTA GCT TTG AGG ACT      351
Gly Ser Ser Pro His Pro Gln Pro Lys Thr Ala Leu Ala Leu Arg Thr
               -20                               -15               -10

TCC TGG ATC TCC TCA GTG TGT TCA GTG ACA CAG CCA CGC CAG ACA TCA      399
Ser Trp Ile Ser Ser Val Cys Ser Val Thr Gln Pro Arg Gln Thr Ser
               -5                               1                   5

AGT CCC ATT ATG CCT TCC GCA TCT TTG ACT TTG ATG ATG ACG      441
Ser Pro Ile Met Pro Ser Ala Ser Leu Thr Leu Met Met Thr
               10                               15                   20

```

(2) INFORMATION FOR SEQ ID NO: 299:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 284 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 2..162
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 9..169
 id N76992
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 162..280
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 168..286
 id N76992
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 2..113
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 8..119
 id W39234
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 173..280
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 176..283
 id W39234
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 113..162
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 118..167
 id W39234
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 20..160
 (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 1..141
id R06371
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 193..280
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 173..260
id R06371
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 159..195
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 138..174
id R06371
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 20..159
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..140
id R06399
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 161..280
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 141..260
id R06399
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 27..165
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..139
id AA043154
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 166..280
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 141..255
id AA043154
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

- (B) LOCATION: 132..215
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq PLSDSWALLPASA/GV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

```

AACAACTTCC GGCCCCACTG AGCGGTGTCC TGAGCCGATT ACAGCTAGGT AGTGGAGCGC      60
CGCTGCTTAC CTGGGTGCAG GAGACAGCCG GAGTCGCTGG GGGAGCTCCG CGCCGCCGGA    120
CGCCCGTGAC C ATG TGG AGG CTG CTG GCT CGC GCT AGT GCG CCG CTC CTG      170
              Met Trp Arg Leu Leu Ala Arg Ala Ser Ala Pro Leu Leu
              -25                               -20

CGG GTG CCC TTG TCA GAT TCC TGG GCA CTC CTC CCC GCC AGT GCT GGC      218
Arg Val Pro Leu Ser Asp Ser Trp Ala Leu Leu Pro Ala Ser Ala Gly
-15                               -10                               -5                               1

GTA AAG ACA CTG CTC CCA GTA CCA AGT TTT GAA GAT GTT TCC ATT CCT      266
Val Lys Thr Leu Leu Pro Val Pro Ser Phe Glu Asp Val Ser Ile Pro
              5                               10                               15

GAA AAA CCC AAG CTA CTG                                          284
Glu Lys Pro Lys Leu Leu
              20

```

(2) INFORMATION FOR SEQ ID NO: 300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 169..332
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 163..326
id H71676
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 92..170
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 87..165
id H71676
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 20..85
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 93
 region 18..83
 id H71676
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 334..364
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 93
 region 330..360
 id H71676
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 264..376
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 3..115
 id AA020192
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 6..347
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.6
 seq ATFVTQALIQXYA/RI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

AAAAA ATG GCG GAT CAT GTG CAG AGC CTG GCC CAA CTA GAG AAT CTG TGC	50
Met Ala Asp His Val Gln Ser Leu Ala Gln Leu Glu Asn Leu Cys	
-110 -105 -100	
AAA CAG CTG TAT GAA ACC ACA GAC ACA RSC AST CGG AGC TCC SAG GCA	98
Lys Gln Leu Tyr Glu Thr Thr Asp Thr Xaa Xaa Arg Ser Ser Xaa Ala	
-95 -90 -85	
GAG AAA GCS TTG GTT GAR TTT ACC AAC AGC CCT GAT TGC CTG AGC AAG	146
Glu Lys Ala Leu Val Glu Phe Thr Asn Ser Pro Asp Cys Leu Ser Lys	
-80 -75 -70	
TGC CAG CTA CTC CTC GAA AGA GGA AGT TCC TCT TAC TCC CAG TTA CTG	194
Cys Gln Leu Leu Glu Arg Gly Ser Ser Ser Tyr Ser Gln Leu Leu	
-65 -60 -55	
GCA GCT ACA TGC CTT ACC AAG CTT GTA TCA CGC ACA AAC AAC CCC CTA	242
Ala Ala Thr Cys Leu Thr Lys Leu Val Ser Arg Thr Asn Asn Pro Leu	
-50 -45 -40	
CCA TTG GAA CAG CGA ATA GAT ATT CGG AAC TAT GTG CTC AAC TAS CTT	290
Pro Leu Glu Gln Arg Ile Asp Ile Arg Asn Tyr Val Leu Asn Xaa Leu	
-35 -30 -25 -20	

GCC ACT CGG CCG AAG TTG GCT ACT TTC GTG ACA CAA GCA CTT ATT CAG 338
Ala Thr Arg Pro Lys Leu Ala Thr Phe Val Thr Gln Ala Leu Ile Gln
 -15 -10 -5

TKA TAT GCC AGA ATC ACA AAA CTG GGC TGG TTT GAC 374
Xaa Tyr Ala Arg Ile Thr Lys Leu Gly Trp Phe Asp
 1 5

(2) INFORMATION FOR SEQ ID NO: 301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 15..235
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 2..222
id H39781
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 16..173
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..158
id AA017398
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 172..235
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 159..222
id AA017398
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 16..235
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..220
id AA059110
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 17..235
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 1..219
 id AA037143
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 56..235
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 56..235
 id R75754
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 14..55
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 15..56
 id R75754
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 62..226
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.6
 seq TCSVCCYLEFWLIA/IP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

```

AACACTTCCT GGTGGATCCG AGTGAGGCGA CGGGGTAGGG GTTGGCGCTC AGGCGGCGAC      60
C ATG GCG TAT CAC GGC CTC ACT GTG CCT CTC ATT GTG ATG AGC GTG TTC      109
Met Ala Tyr His Gly Leu Thr Val Pro Leu Ile Val Met Ser Val Phe
-55 -                      -50                      -45                      -40

TGG GGC TTC GTC GGC TTC TTG GTG CCT TGG TTC ATC CCT AAG GGT CCT      157
Trp Gly Phe Val Gly Phe Leu Val Pro Trp Phe Ile Pro Lys Gly Pro
-35                      -30                      -25

AAC CGG GGA GTT ATC ATT ACC ATG TTG GTG ACC TGT TCA GTT TGC TGC      205
Asn Arg Gly Val Ile Ile Thr Met Leu Val Thr Cys Ser Val Cys Cys
-20                      -15                      -10

TAT CTC TTT TGG CTG ATT GCA ATT CCG GCC TGG                        238
Tyr Leu Phe Trp Leu Ile Ala Ile Pro Ala Trp
-5                      1

```

(2) INFORMATION FOR SEQ ID NO: 302:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 437 base pairs

(B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: complement(397..432)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 283..318
 id H83411
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 54..227
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.5
 seq GGILMGSFQGTIA/GQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

ATATTTGCCC CTTACTTTAT CTTGTGCCTT GAGAAATTGC TGGGGAGAGA GGT ATG	56
Met	
TCC ACT GGG CAG CTG TAC AGG ATG GAG GAT ATA GGG CGT TTC CAC TCC	104
Ser Thr Gly Gln Leu Tyr Arg Met Glu Asp Ile Gly Arg Phe His Ser	
-55 -50 -45	
CAG CAG CCA GGT TCC CTC ACC CCA AGC TCA CCC ACT GTT GGG GAG ATT	152
Gln Gln Pro Gly Ser Leu Thr Pro Ser Ser Pro Thr Val Gly Glu Ile	
-40 -35 -30	
ATC TAC AAT AAC ACC AGA AAC ACA TTG GGG TGG ATT GGG GGT ATC CTT	200
Ile Tyr Asn Asn Thr Arg Asn Thr Leu Gly Trp Ile Gly Gly Ile Leu	
-25 -20 -15 -10	
ATG GGT TCT TTT CAG GGA ACC ATT GCT GGA CAA GGC ACA GGA GCC ACC	248
Met Gly Ser Phe Gln Gly Thr Ile Ala Gly Gln Gly Thr Gly Ala Thr	
-5 1 5	
TCC ATT TCT GAG CTC TGC AAG GGA CAA GAA CTA GAG CCA TCA GGG GCT	296
Ser Ile Ser Glu Leu Cys Lys Gly Gln Glu Leu Glu Pro Ser Gly Ala	
10 15 20	
GGG CTC ACT GTG GCC CCA CCC CAA GCC GTC AGC CTC CAG GGA TCA CAC	344
Gly Leu Thr Val Ala Pro Pro Gln Ala Val Ser Leu Gln Gly Ser His	
25 30 35	
CCT GCC TTG GCT GCT ACA GCT TTT TCA CTC CAS TGC CCT AGG GGA GTT	392
Pro Ala Leu Ala Ala Thr Ala Phe Ser Leu Xaa Cys Pro Arg Gly Val	
40 45 50 55	
CAG CAS CTA ATG ATC TCT ATC TCT GAA CAT CTC TTC ATC CAT GCT	437

Gln Xaa Leu Met Ile Ser Ile Ser Glu His Leu Phe Ile His Ala
60 65 70

(2) INFORMATION FOR SEQ ID NO: 303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 27..347
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..321
id T31485
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 42..352
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..311
id HSC38B061
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 135..325
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 70..260
id T66273
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 69..140
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 5..76
id T66273
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..220
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 6..224

id R24829
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 236..275
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 243..282
id R24829
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 50..318
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 10..278
id HSC2LF071
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 282..332
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq RWWCFHLQAEASA/HP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

```

ATAATAATAT CTAAAAAGCT AAATTTTAAA TACCAGCTTT ACATAAATGA TTGTKGACTC   60
TGGTCTGTKT CTGACACCTT TCCAGAAAAA AGTCAATTGT TCAGGTACAC CAAAGAGGAA   120
GAAGAGCTGT GGAGGCCACC CTCTACAAAG CTTTATAGAA CTTCTGGATC TAACTCACAA   180
ACAAGCTTCC AGAAGAGACT AGAGACCTTA GGCCAGGAGA TGAAGGAGTT CAGTAGCAAA   240
GTCACACCTG TCCAATTCCC TGAGCTTTGC TCACTCAGCT A ATG GGA TGG CAA AGG   296
                                         Met Gly Trp Gln Arg
                                         -15

TGG TGG TGC TTT CAT CTT CAG GCA GAA GCC TCT GCC CAT CCC CCT CAA   344
Trp Trp Cys Phe His Leu Gln Ala Glu Ala Ser Ala His Pro Pro Gln
-10          -5          1

GGG CTG CAG   353
Gly Leu Gln
5

```

(2) INFORMATION FOR SEQ ID NO: 304:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 260 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 80..236

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 95
region 34..190
id N34164
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 91..257

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98
region 66..232
id R89543
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 91..254

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98
region 66..229
id H59647
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 126..170

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.5
seq VIFFACVVRVRDG/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

```

AGGTGACCTG GGCCGAGCCC TCCCGGTCGG CTAAGATTGC TGAGGAGGCG GCGGGTAGCT   60
GGCAGGCGCC GACTTCCGAA GGCCGCCGTC CGGGCGAGGT GTCCTCATGA CTTCTCTTGT   120
GGACC ATG TCC GTG ATC TTT TTT GCC TGC GTG GTA CGG GTA AGG GAT GGA   170
      Met Ser Val Ile Phe Phe Ala Cys Val Val Arg Val Arg Asp Gly
      -15                -10                -5

CTG CCC CTC TCA GCC TCT ACT GAT TTT TAC CAC ACC CAA GAT TTT TTG   218
Leu Pro Leu Ser Ala Ser Thr Asp Phe Tyr His Thr Gln Asp Phe Leu
   1                5                10                15

GAA TGG AGG AGA CGG CTC AAG AGT TTA GCC TTG CGA CTG AAG   260
Glu Trp Arg Arg Arg Leu Lys Ser Leu Ala Leu Arg Leu Lys
      20                25                30

```

(2) INFORMATION FOR SEQ ID NO: 305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 44..210
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 29..195
id R88607
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 17..135
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 16..134
id AA035300
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 136..244
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 134..242
id AA035300
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 38..244
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..207
id AA147873
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(128..244)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 263..379
id AA147836
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: complement(38..131)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 375..468
 id AA147836
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 136..244
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 91..199
 id T69348
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 45..138
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 1..94
 id T69348
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 66..113
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.5
 seq TALAAXTWLGVWG/VR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

```

AATTAGCGCG TAACGCASAG ACTGCTTGCT GCGGCAGAGA CGCCAGAKGT GCAGCTCCAG      60
CAGCA ATG GCA GTG ACG GCG TTG GCG GCG MRG ACG TGG CTT GGC GTG TGG      110
  Met Ala Val Thr Ala Leu Ala Ala Xaa Thr Trp Leu Gly Val Trp
    -15                -10                -5

GGC GTG AGG ACC ATG CAA GCC CGA GGC TTC GGC TCG GAT CAG TCC GAG      158
Gly Val Arg Thr Met Gln Ala Arg Gly Phe Gly Ser Asp Gln Ser Glu
   1                5                10                15

AAT GTC GAC CGG GGC GCG GGC TCC ATC CGG GAA GCC GGT GGG GCC TTC      206
Asn Val Asp Arg Gly Ala Gly Ser Ile Arg Glu Ala Gly Gly Ala Phe
    20                25                30

GGA AAS AGA GAG CAG GCT GAA GAS SAA CGA TAT TTC                        242
Gly Xaa Arg Glu Gln Ala Glu Xaa Xaa Arg Tyr Phe
    35                40

```

(2) INFORMATION FOR SEQ ID NO: 306:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 402 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 151..402

(C) IDENTIFICATION METHOD: fasta

(D) OTHER INFORMATION: identity 100.0
region 1..252
id HSU21128
vrt

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 155..402

(C) IDENTIFICATION METHOD: fasta

(D) OTHER INFORMATION: identity 99.6
region 1..248
id HSU18728
vrt

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 131..402

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 1..272
id H27256
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 161..402

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99
region 31..272
id W95921
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 296..402

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 141..247
id C17793
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 151..252

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98
region 1..102
id C17793
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 174..402
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 1..229
 id AA180902
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 199..402
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 1..204
 id R58323
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 235..288
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 12
 seq FTLFLALIGGTSG/QY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

```

ACATGCCACA CCACAAGATC CCCACAATGA CATAACTCCA TTCAGAGACT GCGTGACTG      60
GGCTGGGTCT CCCCACCCCC CCCTTCAGCT CTTGTATCAC TCAGAATCTG GCAGCCAGTT      120
CCGTCCTGAC AGAGTTCACA GCATATATTG GTGGATTCTT GTCCATAGTG CATCTGCTTT      180
AAGAATTAAC GAAAGCAGTG TCAAGACAGT AAGGATTCAA ACCATTTGCC AAAA ATG      237
                                         Met
AGT CTA AGT GCA TTT ACT CTC TTC CTG GCA TTG ATT GGT GGT ACC AGT      285
Ser Leu Ser Ala Phe Thr Leu Phe Leu Ala Leu Ile Gly Gly Thr Ser
   -15                      -10                      -5
GGC CAG TAC TAT GAT TAT GAT TTT CCC CTA TCA ATT TAT GGG CAA TCA      333
Gly Gln Tyr Tyr Asp Tyr Asp Phe Pro Leu Ser Ile Tyr Gly Gln Ser
   1                      5                      10                      15
TCA CCA AAC TGT GCA CCA GAA TGT AAC TGC CCT GAA AGC TAC CCA AGT      381
Ser Pro Asn Cys Ala Pro Glu Cys Asn Cys Pro Glu Ser Tyr Pro Ser
                20                      25                      30
GCC ATG TAC TGT GAT GAG CTG      402
Ala Met Tyr Cys Asp Glu Leu
                35

```

(2) INFORMATION FOR SEQ ID NO: 307:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 274 base pairs
 (B) TYPE: NUCLEIC ACID

- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 120..272
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 96.1
region 1..151
id HSU21128
vrt

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 124..272
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 96.0
region 1..147
id HSU18728
vrt

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 141..272
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 40..171
id H27256
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 100..136
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..37
id H27256
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 141..272
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 40..171
id W95921
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 141..245
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 52..156
id AA093526

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 89..136
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 2..49
id AA093526
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 145..272
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..128
id AA180902
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 141..223
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 20..102
id C17793
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 206..259
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 12
seq FTLFLALIGGTSG/QY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

```

ATAACTCCAT TCAGAGACTG GCGTGACTGG GCTGGGTCTC CCCACCCCCC CCTTCAGCTC   60
TTGTATGACT CAGAATCTGG CAGCCAGTTC CGTCCTGACA GAGTTCACAG CATATATTGG   120
TGGATTCTTG TCCAWAAGTG GVATCTGCTT TARGAWTTAA CGAAAGCAGT GTCAAGACAG   180
TAAGGATTCA AACCATTTCG CAAAA ATG AGT CTA AGT GCA TTT ACT CTC TTC     232
                               Met Ser Leu Ser Ala Phe Thr Leu Phe
                               -15                               -10

CTG GCA TTG ATT GGT GGT ACC AGT GGC CAG TAC TAT GAT TGG             274
Leu Ala Leu Ile Gly Gly Thr Ser Gly Gln Tyr Tyr Asp Trp
                               -5                               1                               5

```

(2) INFORMATION FOR SEQ ID NO: 308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE

- (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Hypertrophic prostate
- (ix) FEATURE:
- (A) NAME/KEY: other
 - (B) LOCATION: 65..433
 - (C) IDENTIFICATION METHOD: fasta
 - (D) OTHER INFORMATION: identity 100.0
region 1..369
id HSU21128
vrt
- (ix) FEATURE:
- (A) NAME/KEY: other
 - (B) LOCATION: 69..433
 - (C) IDENTIFICATION METHOD: fasta
 - (D) OTHER INFORMATION: identity 99.7
region 1..365
id HSU18728
vrt
- (ix) FEATURE:
- (A) NAME/KEY: other
 - (B) LOCATION: 45..433
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 99
region 1..389
id H27256
est
- (ix) FEATURE:
- (A) NAME/KEY: other
 - (B) LOCATION: 75..433
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 99
region 31..389
id W95921
est
- (ix) FEATURE:
- (A) NAME/KEY: other
 - (B) LOCATION: 210..433
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 99
region 141..364
id C17793
est
- (ix) FEATURE:
- (A) NAME/KEY: other
 - (B) LOCATION: 65..166
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 98
region 1..102
id C17793
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 88..433
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 1..346
 id AA180902
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 113..370
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 1..258
 id R58323
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 149..202
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 12
 seq FTLFLALIGGTSG/QY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

```

AGCTCTTGTA TCACTCAGAA TCTGGCAGCC AGTTCCGTCC TGACAGAGTT CACAGCATAT   60
ATTGGTGGAT TCTTGTCAT AGTGCATCTG CTTTAAGAAT TAACGAAAGC AGTGTCAAGA  120
CAGTAAGGAT TCAAACCATT TGCCAAAA ATG AGT CTA AGT GCA TTT ACT CTC   172
                               Met Ser Leu Ser Ala Phe Thr Leu
                               -15

TTC CTG GCA TTG ATT GGT GGT ACC AGT GGC CAG TAC TAT GAT TAT GAT   220
Phe Leu Ala Leu Ile Gly Gly Thr Ser Gly Gln Tyr Tyr Asp Tyr Asp
-10                -5                1                5

TTT CCG CTA TCA ATT TAT GGG CAA TCA TCA CCA AAC TGT GCA CCA GAA   268
Phe Pro Leu Ser Ile Tyr Gly Gln Ser Ser Pro Asn Cys Ala Pro Glu
                10                15                20

TGT AAC TGC CCT GAA AGC TAC CCA AGT GCC ATG TAC TGT GAT GAG CTG   316
Cys Asn Cys Pro Glu Ser Tyr Pro Ser Ala Met Tyr Cys Asp Glu Leu
                25                30                35

AAA TTG AAA AGT GTA CCA ATG GTG CCT CCT GGA ATC AAG TAT CTT TAC   364
Lys Leu Lys Ser Val Pro Met Val Pro Pro Gly Ile Lys Tyr Leu Tyr
                40                45                50

CTT AGG AAT AAC CAG ATT GAC CAT ATT GAT GAA AAG GCC TTT GAG AAT   412
Leu Arg Asn Asn Gln Ile Asp His Ile Asp Glu Lys Ala Phe Glu Asn
55                60                65                70

GTA ACT GAT CTG CAG TGG CTC GGG   436
Val Thr Asp Leu Gln Trp Leu Gly
                75

```

(2) INFORMATION FOR SEQ ID NO: 309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
(B) LOCATION: 75..345
(C) IDENTIFICATION METHOD: fasta
(D) OTHER INFORMATION: identity 96.3
region 1..269
id HUMD3A07M5
vrt

(ix) FEATURE:

- [illegible]

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 91..150
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.9
seq LLLLLLPFLLYMA/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

AATTTGAATT	GGGGCGTGTCTAGAAAGAGA	AGCCATAGTCTGGCAGCAAC	GCTGGAGCAT	60
CCCCGCTCTGG	TGCCGCTGCA	GCCGGCAGAG	ATG GTT GAG CTC ATG TTC CCG CTG	114
			Met Val Glu Leu Met Phe Pro Leu	
			-20 -15	
TTG CTC CTC CTT CTG CCC TTC CTT CTG TAT ATG GCT GCG CCC CAA ATC				162
Leu Leu Leu Leu Leu Pro Phe Leu Leu Tyr Met Ala Ala Pro Gln Ile				
			-10 -5 1	
AGG AAA ATG CTG TCC AGT GGG GTG TGT ACA TCA ACT GTT CAG CTT CCT				210
Arg Lys Met Leu Ser Ser Gly Val Cys Thr Ser Thr Val Gln Leu Pro				
			5 10 15 20	
GGG AAA GTA GTT GTG GTC ACA GGA GCT AAT ACA GGT ATC GGG AAG GAG				258
Gly Lys Val Val Val Val Thr Gly Ala Asn Thr Gly Ile Gly Lys Glu				
			25 30 35	

ACA GCC AAA GAG CTG GCT CAG AGA GGA GCT CGA GTA TAT KTA GCT TNN	306
Thr Ala Lys Glu Leu Ala Gln Arg Gly Ala Arg Val Tyr Xaa Ala Xaa	
40 45 50	
NGG GAT GTG GAA AAG GGG GAA TTG GTG GCC ARA GAG ATC CAG ACC ACG	354
Xaa Asp Val Glu Lys Gly Glu Leu Val Ala Xaa Glu Ile Gln Thr Thr	
55 60 65	
ACA GGG AAN SAG CAG GTG TTG GTG CGG RAA CTG GAC CTG TCT GAT ACT	402
Thr Gly Xaa Xaa Gln Val Leu Val Arg Xaa Leu Asp Leu Ser Asp Thr	
70 75 80	
AAG TCT ATT CGA GCT TTT GCT	423
Lys Ser Ile Arg Ala Phe Ala	
85 90	

(2) INFORMATION FOR SEQ ID NO: 310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 132..303
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 96
region 1..171
id HSC1R
vrt

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 143..303
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 98
region 24..183
id HUMC1R
vrt

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 181..303
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 1..123
id T74375
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 170..213
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 1..44
id T64778
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 184..228
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.1
seq LLYLLVPALFCRA/GG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

```
AAAAACTCAG ATCTTTTGTT TATGCAAATA GTTCATTCCC TCCAACATTC CTCCGGGAAT   60
GGTCCCCCCT CCACTCCACA GAAAACCCTC CCCTCCCTGC TGTGCATGAC GCGGGCTCCC   120
TCTGSACACA GKGVMCRAAG ACGCTGTCGG GAKAGCCCCA GGATTCAACA CGGGCCTTGA   180
GAA ATG TGG CTC TTG TAC CTC CTG GTG CCG GCC CTG TTC TGC AGG GCA   228
  Met Trp Leu Leu Tyr Leu Val Pro Ala Leu Phe Cys Arg Ala
   -15                -10                -5

GGA GGC TCC ATT CCC ATC CCT CAG AAG TTA TTT GGG GAG GTG ACT TCC   276
Gly Gly Ser Ile Pro Ile Pro Gln Lys Leu Phe Gly Glu Val Thr Ser
   1                5                10                15

CCT CTG TTC CCC AAG CCT TAC CCC AAC GGG   306
Pro Leu Phe Pro Lys Pro Tyr Pro Asn Gly
   20                25
```

(2) INFORMATION FOR SEQ ID NO: 311:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 263 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 50..263
(C) IDENTIFICATION METHOD: fasta
(D) OTHER INFORMATION: identity 99
region 1..214
id HSSPG28
vrt

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 75..263
 (C) IDENTIFICATION METHOD: fasta
 (D) OTHER INFORMATION: identity 99
 region 1..189
 id HSCRISP3G
 vrt

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 51..146
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.7
 seq LLFLVAGLLPSFP/AN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

```

AATATATACG GCTCTAACCT TCTCTCTCTG CACCTTCCTT CTGTCAATAG ATG AAA      56
                                     Met Lys

CAA ATA CTT CAT CCT GCT CTG GAA ACC ACT GCA ATG ACA TTA TTC CCA      104
Gln Ile Leu His Pro Ala Leu Glu Thr Thr Ala Met Thr Leu Phe Pro
-30          -25          -20          -15

GTG CTG TTG TTC CTG GTT GCT GGG CTG CTT CCA TCT TTT CCA GCA AAT      152
Val Leu Leu Phe Leu Val Ala Gly Leu Leu Pro Ser Phe Pro Ala Asn
          -10          -5          1

GAA GAT AAG GAT CCC GCT TTT ACT GCT TTG TTA ACC ACC CAA ACA CAA      200
Glu Asp Lys Asp Pro Ala Phe Thr Ala Leu Leu Thr Thr Gln Thr Gln
          5          10          15

GTG CAA AGG GAG ATT GTG AAT AAG CAC AAT GAA CTG AGG AGA GCA GTA      248
Val Gln Arg Glu Ile Val Asn Lys His Asn Glu Leu Arg Arg Ala Val
          20          25          30

TCT CCC CCT GCC AAA      263
Ser Pro Pro Ala Lys
          35

```

(2) INFORMATION FOR SEQ ID NO: 312:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 465 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 133..467

(C) IDENTIFICATION METHOD: fasta
(D) OTHER INFORMATION: identity 97
region 1..335
id HSU03877
vrt

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 213..467
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 232..486
id AA150097
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 35..204
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 55..224
id AA150097
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 43..467
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 56..480
id AA155808
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 43..404
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 73..434
id AA147966
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 395..467
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 424..496
id AA147966
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 51..467
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..417
id AA058479
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 70..405
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 1..336
 id W46890
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 394..425
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 326..357
 id W46890
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 52..102
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.9
 seq LFLTMLTLALVKS/QD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

```

AACTCCCTC GCTGCCCGG CCCGGAGCGC ASSNGGCCGC ACAGATTCAC A ATG TTG      57
                                     Met Leu

AAA GCC CTT TTC CTA ACT ATG CTG ACT CTG GCG CTG GTC AAG TCA CAG      105
Lys Ala Leu Phe Leu Thr Met Leu Thr Leu Ala Leu Val Lys Ser Gln
-15                      -10                      -5                      1

GAC ACC GAA GAA ACC ATC ACG TAC ACG CAA TGC ACT GAC GGA TAT GAG      153
Asp Thr Glu Glu Thr Ile Thr Tyr Thr Gln Cys Thr Asp Gly Tyr Glu
                    5                      10                      15

TGG GAT CCT GTG AGA CAG CAA TGC AAA GAT ATT GAT GAA TGT GAC ATT      201
Trp Asp Pro Val Arg Gln Gln Cys Lys Asp Ile Asp Glu Cys Asp Ile
                20                      25                      30

GTC CCA GAC GCT TGT AAA GGT GGA ATG AAG TGT GTC AAC CAC TAT GGA      249
Val Pro Asp Ala Cys Lys Gly Gly Met Lys Cys Val Asn His Tyr Gly
                35                      40                      45

GGA TAC CTC TGC CTT CCG AAA ACA GCC CAG ATT ATT GTC AAT AAT GAA      297
Gly Tyr Leu Cys Leu Pro Lys Thr Ala Gln Ile Ile Val Asn Asn Glu
                50                      55                      60                      65

CAG CCT CAG CAG GAA ACA CAA CCA GCA GAA GGA ACC TCA GGG GCA ACC      345
Gln Pro Gln Gln Glu Thr Gln Pro Ala Glu Gly Thr Ser Gly Ala Thr
                    70                      75                      80

ACC GGG GTT GTA GCT GCC DNC AGC ATG GCA ACC AGT GBA GTG TTG MNN      393
Thr Gly Val Val Ala Ala Xaa Ser Met Ala Thr Ser Xaa Val Leu Xaa
                    85                      90                      95

GGG GGT GGT TTT GTG GCC AGT GCT GCT GCA GTC GCA GGC CCT GAA ATG      441
Gly Gly Gly Phe Val Ala Ser Ala Ala Ala Val Ala Gly Pro Glu Met
                100                      105                      110

```

CAG ACT GGC CGG AAT AAC TTT GTC
Gln Thr Gly Arg Asn Asn Phe Val
115 120

465

(2) INFORMATION FOR SEQ ID NO: 313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..256
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 96
region 1..204
id HUMTCAYV
vrt

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..256
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 93
region 1..207
id MACTCRAAQ
vrt

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..256
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 94
region 1..204
id MACTCRAAR
vrt

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 50..115
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq LLILWFHLDVCSS/IL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

AATTTTGGCT GCAAAACGTT TTTCTGCTGT GGGTACGTGA GCAGGAAAC ATG GAG AAG 58
Met Glu Lys
-20

AAT CCT TTG GCA GCC CCA TTA CTA ATC CTC TGG TTT CAT CTT GAC TGC	106
Asn Pro Leu Ala Ala Pro Leu Leu Ile Leu Trp Phe His Leu Asp Cys	
-15 -10 -5	
GTG AGC AGC ATA CTG AAC GTG GAA CAA AGT CCT CAG TCA CTG CAT GTT	154
Val Ser Ser Ile Leu Asn Val Glu Gln Ser Pro Gln Ser Leu His Val	
1 5 10	
CAG GAG GGA GAC AGC ACC AAT TTC ACC TGC AGC TTC CCT TCC AGC AAT	202
Gln Glu Gly Asp Ser Thr Asn Phe Thr Cys Ser Phe Pro Ser Ser Asn	
15 20 25	
TTT TAT GCC TTA CAC TGG TAC AGA TGG GAA ACT GCA AAA AGC CCC GAG	250
Phe Tyr Ala Leu His Trp Tyr Arg Trp Glu Thr Ala Lys Ser Pro Glu	
30 35 40 45	
GCC GTG	256
Ala Val	

(2) INFORMATION FOR SEQ ID NO: 314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 62..455
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 98.7
region 1..392
id HSU32907
vrt

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 138..415
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..278
id H09504
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 410..454
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 274..318
id H09504

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 160..455
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..296
id H17686
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 128..329
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 42..243
id AA247900
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 85..123
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 1..39
id AA247900
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 318..355
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 231..268
id AA247900
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 128..231
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 22..125
id R57541
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 231..274
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 124..167
id R57541
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 312..455
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 1..144
id N87278
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 345..389
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3
seq VVTIVILLCFCKA/AE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

```
AGCTGGGGCC ATGTAATTTA AAACCTCTGA AAAGTGTGCT GCGGTCCGTG CACAGCATT 60
GTATAACGTG AGGGCTGAAT GCAGCCCATT CTCTGGAGAA CTCCTCACA CACCGCAGCM 120
AARGAGAAGG MCTGAAAGAC AAACCTGGGT GCAGCCAGAG AGGTCCAGAT AGATGAGCTT 180
GTGGCATCCA TTCCCCAAGT TCAGCCTAGG GACTCCACGT ACCCCAGCTG GGTCTCATTG 240
TTCCAGAACT GCATTAGTTA AGATTACCCA GACTTNGATT TCAAAGGAAT ACTTTCATTG 300
TTCCGTCTGT AACACGAAGT AATTGGGGCC AGCTGGATGT CAGG ATG CGT GTG GTT 356
                                         Met Arg Val Val
                                         -15

ACC ATT GTA ATC TTG CTC TGC TTT TGC AAA GCG GCT GAG CTG CGC AAA 404
Thr Ile Val Ile Leu Leu Cys Phe Cys Lys Ala Ala Glu Leu Arg Lys
-10                               -5                               1                               5

GCA AGC CCA GGC AGT GTG AGA AGC CGA GTG AAT CAT GGC CGG GCG GGT 452
Ala Ser Pro Gly Ser Val Arg Ser Arg Val Asn His Gly Arg Ala Gly
10                               15                               20

GGA 455
Gly
```

(2) INFORMATION FOR SEQ ID NO: 315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 45..438
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 100
region 1..394

id HSU20350
vrt

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 87..438
(C) IDENTIFICATION METHOD: fasta
(D) OTHER INFORMATION: identity 99
region 3..352
id HSU28934
vrt

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 132..401
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.1
seq LLFVATLPFWTHY/LI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

```

AAACTCTGCA AATAAAATGC TCTTAGAGGG AAGGAAAGGG AAATACTCGT CTCTGGTAAA      60
GTCTGAGCAG GACAGGGTGG CTGACTGGCA GATCCAGAGG TTCCCTTGGC AGTCCACGCC      120
AGGCCTTCAC C ATG GAT CAG TTC CCT GAA TCA GTG ACA GAA AAC TTT GAG      170
           Met Asp Gln Phe Pro Glu Ser Val Thr Glu Asn Phe Glu
           -90                      -85                      -80

TAC GAT GAT TTG GCT GAG GCC TGT TAT ATT GGG GAC ATC GTG GTC TTT      218
Tyr Asp Asp Leu Ala Glu Ala Cys Tyr Ile Gly Asp Ile Val Val Phe
           -75                      -70                      -65

GGG ACT GTG TTC CTG TCC ATA TTC TAC TCC GTC ATC TTT GCC ATT GGC      266
Gly Thr Val Phe Leu Ser Ile Phe Tyr Ser Val Ile Phe Ala Ile Gly
           -60                      -55                      -50

CTG GTG GGA AAT TTG TTG GTA GTG TTT GCC CTC ACC AAC AGC AAG AAG      314
Leu Val Gly Asn Leu Leu Val Val Phe Ala Leu Thr Asn Ser Lys Lys
           -45                      -40                      -35

CCC AAG AGT GTC ACC GAC ATT TAC CTC CTG AAC CTG GCC TTG TCT GAT      362
Pro Lys Ser Val Thr Asp Ile Tyr Leu Leu Asn Leu Ala Leu Ser Asp
           -25                      -20                      -15

CTG CTG TTT GTA GCC ACT TTG CCC TTC TGG ACT CAC TAT TTG ATA AAT      410
Leu Leu Phe Val Ala Thr Leu Pro Phe Trp Thr His Tyr Leu Ile Asn
           -10                      -5                      1

GAA AAG GGC CTC CAC AAT GCC ATG TGC      437
Glu Lys Gly Leu His Asn Ala Met Cys
           5                      10

```

(2) INFORMATION FOR SEQ ID NO: 316:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids
(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -23..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 11.4
seq VLALLLFVHYSNG/DE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

Met Val Phe Val His Leu Tyr Leu Gly Asn Val Leu Ala Leu Leu Leu
-20 -15 -10

Phe Val His Tyr Ser Asn Gly Asp Glu Ser Ser Asp Pro Gly Pro Gln
-5 1 5

His Arg Ala
10

(2) INFORMATION FOR SEQ ID NO: 317:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -29..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 11.3
seq FLLCIFLICAALA/AQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

Met Gly Met Cys Phe Ala Ala Glu Ser Asp Val Gln Met Phe Ile Ala
-25 -20 -15

Phe Leu Leu Cys Ile Phe Leu Ile Cys Ala Ala Leu Ala Ala Gln Lys
-10 -5 1

Ser Gly
5

(2) INFORMATION FOR SEQ ID NO: 318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11
seq VLFLFLFWGVSLA/GS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

Met Ala Val Arg Glu Leu Cys Phe Ser Arg Gln Arg Gln Val Leu Phe
-25 -20 -15

Leu Phe Leu Phe Trp Gly Val Ser Leu Ala Gly Ser Gly Phe Gly Arg
-10 -5 1 5

Tyr Ser Val Thr Gly
10

(2) INFORMATION FOR SEQ ID NO: 319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.7
seq LILLALATGLVGG/ET

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu Val
-15 -10 -5

Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro His Ser
 1 5 10

Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly
 15 20 25 30

Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu
 35 40 45

Lys Pro Arg Tyr Gly
 50

(2) INFORMATION FOR SEQ ID NO: 320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.7
seq LILLALATGLVGG/ET

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu Val
 -15 -10 -5

Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro His Xaa
 1 5 10

Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly
 15 20 25 30

Ala Thr Leu Ile Ala Pro Arg Trp Leu
 35

(2) INFORMATION FOR SEQ ID NO: 321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
 (B) LOCATION: -30..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 10.6
 seq SLLLAVLVFFLFA/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

```

Met Arg Ser Cys Leu Trp Arg Cys Arg His Leu Ser Gln Gly Val Gln
-30                -25                -20                -15

Trp Ser Leu Leu Leu Ala Val Leu Val Phe Phe Leu Phe Ala Leu Pro
          -10                -5                1

Ser Xaa Xaa Xaa Xaa Xaa Gln Thr Lys Pro Ser Arg His Gln Arg Thr
      5                10                15

Glu Asn Ile Lys Glu Arg Ser Leu Xaa Ser Leu Ala Lys Pro Lys Ser
  20                25                30

Gln Ala Pro Thr Arg Ala Arg Arg Thr Thr Ile Tyr Ala Glu Pro Val
  35                40                45                50

Pro Glu Asn Asn Ala Leu Asn Thr Gln Thr Gln Pro Lys Ala His Thr
          55                60                65

Thr Gly Asp Arg Arg Lys Gly
      70
  
```

(2) INFORMATION FOR SEQ ID NO: 322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
 (B) LOCATION: -18..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 10.6
 seq XILLALATGLVGG/EI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

```

Met Arg Ile Leu Gln Xaa Ile Leu Leu Ala Leu Ala Thr Gly Leu Val
  
```

-15					-10					-5					
Gly	Gly	Glu	Ile	Arg	Ile	Ile	Lys	Gly	Phe	Glu	Cys	Lys	Pro	His	Ser
		1				5					10				
Gln	Pro	Trp	Gln	Ala	Ala	Leu	Phe	Glu	Lys	Thr	Arg	Leu	Leu	Leu	Trp
15					20					25					30
Gly	Asp	Ala	His	Arg	Pro	Gln	Met	Ala	Pro	Asp	Ser	Ser	Pro	Leu	Pro
				35					40					45	
Gln	Ala	Pro	Leu	His	Ser	Ser	Pro	Gly	Ala	Ala	Gln	Pro	Pro	Glu	Gly
			50					55					60		

(2) INFORMATION FOR SEQ ID NO: 323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -38..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 10.4
seq LWLLKLKVSTXWA/VR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

Met Leu Glu Glu Cys Gly Ala Gly Val Asp Leu Gly Phe Gly Gly Val
-35 -30 -25
-
Lys Phe Ala Ser Glu Thr Pro Asn Leu Leu Trp Leu Leu Leu Lys Leu
-20 -15 -10
Val Ser Thr Xaa Trp Ala Val Arg Val Thr Leu Ile Ile Phe Asn Asn
-5 1 5 10
Gln Ala Arg

(2) INFORMATION FOR SEQ ID NO: 324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Normal prostate

- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -23..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 10.2
 seq RCLLLALVAESSS/QT

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

Met Ile Ala Cys Ser Ile Arg Glu Leu His Arg Cys Leu Leu Leu Ala
 -20 -15 -10

Leu Val Ala Glu Ser Ser Ser Gln Thr His Gly
 -5 1

(2) INFORMATION FOR SEQ ID NO: 325:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -17..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 10.2
 seq SLVLCLLSATVFS/LQ

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

Met Gly Pro Pro Ser Leu Val Leu Cys Leu Leu Ser Ala Thr Val Phe
 -15 -10 -5

Ser Leu Gln Gly Gly Ser Ser Ala Phe Leu Ser His His Arg Pro Gly
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 326:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 112 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(F) TISSUE TYPE: Hypertrophic prostate

seq AMWWLLWGV LQX/XP

Gly Leu Cys His Asn Leu Ile Arg Arg Phe Gly Ser Lys Pro Leu Gly
65 70 75

(D) TOPOLOGY: LINEAR

(F) TISSUE TYPE: Normal prostate

seq LLTLALLGGPTWX/XX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

Met His Arg Pro Glu Ala Met Leu Leu Leu Thr Leu Ala Leu Leu
 -20 -15 -10

Gly Gly Pro Thr Trp Xaa Xaa Lys Met Tyr Gly Pro Gly Gly Gly Lys
 -5 1 5 10

Tyr Phe Ser Thr Thr Glu Asp Tyr Asp His Glu Ile Thr Gly Leu Arg
 15 20 25

Val Ser Val Gly Xaa Leu Leu Val Lys Ser Val Gln Val Lys Leu Gly
 30 35 40

Asp Ser Trp Asp Val Lys Leu Gly Gly Leu Arg Trp Glu Tyr Pro Gly
 45 50 55

Ser His Pro Ala Ala Arg Arg Ile His His Lys Ser Leu Cys Arg Phe
 60 65 70

Gln Ala Phe Leu
 75

(2) INFORMATION FOR SEQ ID NO: 328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.6
 seq SVSLALLSGWVGS/RQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

Met Val Ser Val Ser Leu Ala Leu Leu Ser Gly Trp Val Gly Ser Arg
 -15 -10 -5 1

Gln Gly Gly Val Gly Leu Ser Thr Leu Val Thr Leu Gly Leu Val Ser
 5 10 15

Trp Cys Trp Arg Met Val Arg Thr Gln Ala Leu Glu Gly Phe Leu Ser
 20 25 30

Val Lys Tyr Tyr Ser Ala Phe Ser Ala Asp Leu
 35 40

(2) INFORMATION FOR SEQ ID NO: 329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -49..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.5
seq IVFLLLRVSPCLG/PS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

Met His Ile Phe Ser Ile Cys Cys Met Xaa Ser Glu Leu His Lys Met
 -45 -40 -35

Lys Ser Leu Ser Leu Gln Leu Ala Ser Glu Lys Arg Ser Leu Val Ala
 -30 -25 -20

Leu Val Glu Glu Ile Val Phe Leu Leu Leu Arg Val Ser Pro Cys Leu
 -15 -10 -5

Gly Pro Ser Xaa Lys Pro Arg
 1 5

(2) INFORMATION FOR SEQ ID NO: 330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.3
seq VSALLMAWFGVLS/CV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

Met Lys Leu Trp Val Ser Ala Leu Leu Met Ala Trp Phe Gly Val Leu
 -15 -10 -5

Ser Cys Val Gln Thr Gly
 1 5

(2) INFORMATION FOR SEQ ID NO: 331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.3
seq LLLPLMLMSMVSS/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

Met Lys Val Leu Ile Ser Ser Leu Leu Leu Leu Leu Pro Leu Met Leu
 -20 -15 -10

Met Ser Met Val Ser Ser Ser Leu Xaa Pro Gly Val Ala Arg Gly His
 -5 1 5 10

Arg Asp Arg Gly Gln Ala Ser Arg Arg Trp Leu Gln Glu Gly Gly Leu
 15 20 25

(2) INFORMATION FOR SEQ ID NO: 332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.3
seq LLLPLMLMSW/SS/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

Met Lys Val Leu Ile Ser Ser Leu Leu Leu Leu Pro Leu Met Leu
 -20 -15 -10

Met Ser Met Val Ser Ser Ser Leu Asn Pro Gly Val Ala Arg Gly His
 -5 1 5 10

Arg Asp Arg Gly Gln Ala Ser Arg Arg Trp Leu Gln Glu Gly Gly Gln
 15 20 25

Glu Cys Glu Cys Lys Asp Trp Phe Leu Arg Ala Pro Arg Arg Lys Phe
 30 35 40

Met Thr Val Ser Gly
 45

(2) INFORMATION FOR SEQ ID NO: 333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.2
seq LLLQLSLPSPTS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

Met Leu Leu Leu Leu Gln Leu Ser Leu Pro Ser Pro Thr Ser Ser Pro
 -10 -5 1

(2) INFORMATION FOR SEQ ID NO: 334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.1
seq LSFKLLLLAVALG/FF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

Met Leu Lys Met Leu Ser Phe Lys Leu Leu Leu Leu Ala Val Ala Leu
-15 -10 -5

Gly Phe Phe Glu Gly Asp Ala Lys Phe Gly Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8
seq LLTLALLGXXXWA/GK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

Met His Arg Pro Glu Ala Met Leu Leu Leu Leu Thr Leu Ala Leu Leu
-20 -15 -10

Gly Xaa Xaa Xaa Trp Ala Gly Lys Met Tyr Gly Pro Gly Gly Gly Lys
-5 1 5 10

Tyr Phe Ser Thr Thr Glu Asp Tyr Asp His Glu Ile Thr Gly Leu Arg
15 20 25

Val Ser Val Gly Leu Leu Leu Val Lys Ser Val Gln Val Lys Leu Gly
30 35 40

Asp Ser Trp Asp Val
45

(2) INFORMATION FOR SEQ ID NO: 336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids

(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -16..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8
seq VSAVLCVCAAAWC/SQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

```
Met Leu Lys Val Ser Ala Val Leu Cys Val Cys Ala Ala Ala Trp Cys
-15                      -10                      -5

Ser Gln Ser Leu Ala Ala Ala Ala Val Ala Ala Ala Gly Gly Arg
 1                      5                      10                      15

Ser Asp Gly Gly Asn Phe Leu Asp Asp Lys Gln Trp Leu Thr Thr Ile
                20                      25                      30

Ser Gln Tyr Asp Lys Glu Val Gly Gln Trp Asn Lys Phe Arg Asp Asp
                35                      40                      45

Asp Tyr Phe Arg Thr Gly
 50
```

(2) INFORMATION FOR SEQ ID NO: 337:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -17..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.8
seq VLWLISFFTFDTG/HG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

```
Met Lys Val Gly Val Leu Trp Leu Ile Ser Phe Phe Thr Phe Thr Asp
-15                      -10                      -5
```

Gly His Gly Gly Phe Leu Gly Lys Asn Asp Gly Ile Lys Thr Lys Lys
1 5 10 15
Glu Leu Ile Val Asn Lys Lys Lys His Leu Gly Leu Gly
20 25

(2) INFORMATION FOR SEQ ID NO: 338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.7
seq ILDDLICLLFITA/CV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

Met Cys Ile Ile Leu Leu Asp Leu Ile Cys Leu Leu Phe Ile Thr Ala
-15 -10 -5
Cys Val Gly
1

(2) INFORMATION FOR SEQ ID NO: 339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -59..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6
seq FMVFGSFFPLISC/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

Met Asp Cys Ala Ser Ile Ser Val Lys Phe Thr Ser Met Ala Thr Met
 -55 -50 -45

His Asp Leu Ser Gln Phe Trp Ala Ser Arg Gly Glu Val Thr Asn Trp
 -40 -35 -30

Trp Pro Val Gly Gln Thr Ser Leu Pro Leu Phe Tyr Leu Ala Phe Met
 -25 -20 -15

Val Phe Gly Ser Phe Phe Pro Leu Ile Ser Cys Gln Pro Gly
 -10 -5 1

(2) INFORMATION FOR SEQ ID NO: 340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6
seq LVVLFGITAGATG/AK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

Met Thr Ala Ser Pro Asp Tyr Leu Val Val Leu Phe Gly Ile Thr Ala
 -20 -15 -10 -5

Gly Ala Thr Gly Ala Lys Leu Gly Ser Asp Glu Lys Glu Leu Ile Leu
 1 5 10

Leu Phe Trp Lys Val Val Asp Leu Ala Asn Lys Lys Val Gly Gln Leu
 15 20 25

His Glu Xaa Xaa Leu Asp Arg Ile Trp
 30 35

(2) INFORMATION FOR SEQ ID NO: 341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6
seq CVLVLAAAAGAVA/VF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

```

Met Val Cys Val Leu Val Leu Ala Ala Ala Gly Ala Val Ala Val
-15          -10          -5          1

Phe Leu Ile Leu Arg Ile Trp Val Val Leu Arg Ser Met Asp Val Thr
      5          10          15

Pro Arg Glu Ser Leu Ser Ile Leu Val Val Ala Gly Ser Gly Gly His
      20          25          30

Thr Thr Glu Ile Leu Arg Leu Leu Gly Ser Leu Ser Asn Ala Tyr Ser
      35          40          45

Pro Arg His Tyr Val Ile Ala Asp Thr Asp Glu Met Ser Ala Thr
      50          55          60

```

(2) INFORMATION FOR SEQ ID NO: 342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -44..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.5
seq LMIPLLLTPITA/TS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

```

Met Lys Lys Thr Gly Asp Gly Gly Thr Leu Ser Thr Glu Arg Ile Gly
      -40          -35          -30

Gly Ala Ala Leu Leu Ser Leu Leu Leu Lys Arg Met Lys Met Thr Leu
      -25          -20          -15

```

WO 99/06550

374

Met Ile Pro Leu Leu Leu Leu Thr Pro Ile Thr Ala Thr Ser Thr Ser
 -10 -5 1
 Arg Trp Pro Glu Ile Gly Val Val Ala Ile Arg Ser Gln Leu Arg Ala
 5 10 15 20
 Leu His Thr Cys Gly Gln Glu Pro Val Pro Ala Met Gly Ser Glu Gly
 25 30 35
 Ala Ala

(2) INFORMATION FOR SEQ ID NO: 343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.5
seq LTFLLQLLISSLP/RE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

Met Glu Leu Gly Cys Trp Thr Gln Leu Gly Leu Thr Phe Leu Gln Leu
 -20 -15 -10
 Leu Leu Ile Ser Ser Leu Pro Arg Glu Tyr Thr Val Ile Asn Glu Ala
 -5 1 5
 Cys Pro Gly Ala Glu Trp Xaa Ile Met Cys Arg Glu Cys Cys Glu Tyr
 10 15 20 25
 Asp Gln Ile Glu Cys Val Cys Pro Gly Lys Arg Glu Val Val Gly Tyr
 30 35 40
 Thr Ile Pro Cys Cys Arg Asn Glu Xaa Asn Glu Cys Asp Ser Cys Leu
 45 50 55
 Ile His Pro Gly Cys Thr Ile Phe Glu Asn Cys Xaa Ser Cys Arg Asn
 60 65 70
 Gly Ser Trp Gly Gly Thr Leu
 75 80

(2) INFORMATION FOR SEQ ID NO: 344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2
seq SLLFFLLLEGGXT/EQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

Met Arg Xaa Lys Trp Lys Met Gly Gly Met Lys Tyr Ile Phe Ser Leu
-25 -20 -15

Leu Phe Phe Leu Leu Leu Glu Gly Gly Xaa Thr Glu Gln Val Xaa His
-10 -5 1 5

Ser Glu Thr Tyr Cys Met Phe Gln Asp Lys Lys Tyr Arg Val Gly Glu
10 15 20

Arg Trp His Pro Tyr Leu Glu Pro Tyr Gly Leu Val Tyr Cys Val Asn
25 30 35

Cys Ile Cys Ser Glu Xaa Gly Asn Val Leu Cys Ser Arg Val Arg Cys
40 45 50

(2) INFORMATION FOR SEQ ID NO: 345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2
seq VSIMLLLVTVSDC/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

Met Arg Gly Ala Thr Arg Val Ser Ile Met Leu Leu Leu Val Thr Val
 -15 -10 -5

Ser Asp Cys Ala Val Ile Thr Gly Ala Cys Glu Arg Asp Val Gln Cys
 1 5 10

Gly Ala Gly Thr Cys Cys Ala Ile Ser Leu Trp Leu Arg Gly Leu Arg
 15 20 25

Met Cys Thr Pro Leu Gly Arg Glu Gly Glu Glu Cys His Pro Gly Ser
 30 35 40 45

His Lys Ile Pro Phe Phe Arg Lys Arg Lys His His Thr Cys Pro Cys
 50 55 60

Leu

(2) INFORMATION FOR SEQ ID NO: 346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2
seq SALLFSSLCEAST/VV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

Met Ile Ala Ile Ser Ala Val Ser Ser Ala Leu Leu Phe Ser Leu Leu
 -20 -15 -10

Cys Glu Ala Ser Thr Val Val Leu Leu Asn Ser Thr Asp Ser Ser Pro
 -5 1 5 10

Xaa Thr Asn Asn Phe Xaa Asp Xaa Glu Ala Ala Leu Lys Ala His
 15 20 25

(2) INFORMATION FOR SEQ ID NO: 347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2
seq SALLFSLLEAST/VV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

Met Ile Ala Ile Ser Ala Val Ser Ser Ala Leu Leu Phe Ser Leu Leu
-20 -15 -10

Cys Glu Ala Ser Thr Val Val Leu Leu Asn Ser Thr Asp Ser Ser Pro
-5 1 5 10

Pro Thr Asn Asn Phe Thr Asp Ile Glu Ala Ala Leu Lys Ala Gln Leu
15 20 25

Asp Ser Ala Asp Ile Pro Lys Ala Arg Arg Lys Arg Tyr Ile Ser Gln
30 35 40

Asn Asp Met Ile Ala Ile Leu Asp Tyr His Asn Gln Val Arg Gly Lys
45 50 55

Val Phe Pro Xaa Ala
60

(2) INFORMATION FOR SEQ ID NO: 348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2
seq LLTLVLCVAVAYE/RQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

Met Asp Pro Asn Gly Gly Cys Cys Thr Leu Leu Thr Leu Val Leu Cys
-20 -15 -10

Val Ala Val Ala Tyr Glu Arg Gln Glu
-5 1

(2) INFORMATION FOR SEQ ID NO: 349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2
seq LFTFSTSLPSSLS/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

Met Glu Gly Glu Ile Tyr Phe Gln Val Phe Leu Ser Leu Phe Thr Phe
-25 -20 -15 -10

Ser Thr Ser Leu Pro Ser Ser Leu Ser Ser Ser Ser Leu Ser Ser Ser
-5 1 5

Asn Gly

(2) INFORMATION FOR SEQ ID NO: 350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -41..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7
seq FLCMLAAIDLALS/TS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

Met Tyr Val Val Ala Met Phe Gly Asn Cys Ile Val Val Phe Ile Val
 -40 -35 -30

Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met
 -25 -20 -15 -10

Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met
 -5 1

(2) INFORMATION FOR SEQ ID NO: 351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -43..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7
seq PWFLAPWCPTQS/NR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

Met Arg Glu Thr Xaa Pro Leu Pro Lys Pro Leu Lys Asp Thr Ala Pro
 -40 -35 -30

Ser Ser His Gly Val Gly Ser Asp Ser Pro Ser Ala Thr Arg Pro Trp
 -25 -20 -15

Phe Leu Ala Pro Trp Cys Pro Gly Thr Gln Ser Asn Arg Ile Cys His
 -10 -5 1 5

Pro Pro Leu Ser Ser Pro Pro Asp Gln Ala Thr Cys Leu Arg Gly
 10 15 20

(2) INFORMATION FOR SEQ ID NO: 352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -60..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7
seq VLVVLALRSLGRS/CS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

```

Met Asp Arg Pro Gly Ser Leu Ser Val Phe Gly Ser Leu Pro Ala Ser
-60                               -55                               -50                               -45

Leu Gly Thr Trp Leu Ser Ser Pro Ala Trp Leu Val Asp Arg Pro Val
                               -40                               -35                               -30

Arg Ser Ala His Pro Ser Ala Asn Ser Thr Gly Val Arg Met Ser Val
                               -25                               -20                               -15

Leu Val Val Leu Ala Leu Arg Ser Leu Gly Arg Ser Cys Ser Leu Ser
                               -10                               -5                               1

Gln Ala Ala Pro Ser Arg Trp Thr Arg Ser Asn Asp Ala Pro Gln Pro
5                               10                               15                               20

Pro Gly Ser Gln His Ile Phe His Thr Xaa Val Pro Gly
                               25                               30

```

(2) INFORMATION FOR SEQ ID NO: 353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7
seq VILLFSYPSCCLC/FL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

```

Met His Tyr Phe Val Ala Gly Lys Val Ile Leu Leu Phe Ser Tyr Pro
-20                               -15                               -10

Ser Cys Cys Leu Cys Phe Leu Val Tyr Arg Arg Val Ser Xaa Leu Phe
-5                               1                               5                               10

Lys Cys Phe Glu
                               15

```

(2) INFORMATION FOR SEQ ID NO: 354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7
seq STVVVLQVLTQATS/QD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

Met Asp Leu Asn Ser Ala Ser Thr Val Val Leu Gln Val Leu Thr Gln
 -15 -10 -5

Ala Thr Ser Gln Asp Thr Ala Val Leu Lys Pro Ala Glu Glu Gln Leu
 1 5 10

Lys Gln Trp Glu Thr Gln Pro Gly Phe Tyr Ser Val Leu Leu Asn Ile
 15 20 25

Phe Thr Asn His Gly
 30

(2) INFORMATION FOR SEQ ID NO: 355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -73..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7
seq FLCMLAAIDLALS/TS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

```

Met Ser Ser Cys Asn Phe Thr His Ala Thr Phe Val Leu Ile Gly Ile .
      -70              -65              -60

Pro Gly Leu Glu Lys Ala His Phe Trp Val Gly Phe Pro Leu Leu Ser
      -55              -50              -45

Met Tyr Val Val Ala Met Phe Gly Asn Cys Ile Val Val Phe Ile Val
      -40              -35              -30

Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met
      -25              -20              -15              -10

Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met
      -5              1

```

(2) INFORMATION FOR SEQ ID NO: 356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -56..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9
seq PLFFSCSISATHS/CV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

```

Met Tyr Arg Leu Ser Leu Ile Ala Gly Pro Gly Ser Tyr Pro Val Leu
      -55              -50              -45

Arg Trp Gly Val Trp Asp Ile Pro Ser Ser Leu Val Gln Val Thr Tyr
      -40              -35              -30              -25

His Gln Pro Asn Leu Thr Thr Asn Leu Asp Leu Pro Leu Phe Phe Ser
      -20              -15              -10

Cys Ser Ile Ser Ala Thr His Ser Cys Val Lys Pro Pro Ser Val Ile
      -5              1              5

Ile Gly Ile Ser Ser Phe Leu Ser Phe Pro Tyr Gln Thr Leu Val
      10              15              20

```

(2) INFORMATION FOR SEQ ID NO: 357:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 91 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -24..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.9
 seq LCFLLLAVAMSFF/GS
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

Met Leu Val Asp Gly Pro Ser Glu Arg Pro Ala Leu Cys Phe Leu Leu
 -20 -15 -10

Leu Ala Val Ala Met Ser Phe Phe Gly Ser Ala Leu Ser Ile Asp Glu
 -5 1 5

Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg Leu Gly Gly
 10 15 20

Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu Arg Leu Met
 25 30 35 40

Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr Leu Ile Phe
 45 50 55

Pro Pro Ser Met His Phe Phe Gln Ala Lys Trp
 60 65

(2) INFORMATION FOR SEQ ID NO: 358:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Cancerous prostate
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -35..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.9
 seq XLXXLLTPPPSYG/HQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

```

Met Pro Cys Ser Leu Thr Trp Arg Leu Pro Pro Arg Thr Cys Gln Xaa
-35                -30                -25                -20

Xaa Gly Leu Xaa Lys Ser Xaa Leu Xaa Xaa Leu Leu Thr Pro Pro Pro
-15                -10                -5

Ser Tyr Gly His Gln Pro Gln Thr Gly Ser Gly Glu Ser Xaa Gly Ala
      1                5                10

Ser Gly Asp Lys Asp His Leu Tyr Ser Thr Val Cys
      15                20                25

```

(2) INFORMATION FOR SEQ ID NO: 359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -41..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.8
seq LFLFLTSIAEXCS/TP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

```

Met Val Xaa Trp Leu Val Leu Phe Ala Leu Gln Ile Tyr Ser Tyr Xaa
-40                -35                -30

Ser Thr Arg Asp Gln Pro Ala Ser Arg Xaa Arg Leu Leu Phe Leu Phe
-25                -20                -15                -10

Leu Thr Ser Ile Ala Glu Xaa Cys Ser Thr Pro Tyr Ser Leu Leu Gly
      -5                1                5

Xaa Val Phe Thr Val Ser Phe Val Ala Leu Gly Val Leu Thr Leu Cys
      10                15                20

Lys Phe Tyr Leu Gln Gly Tyr Arg Ala Phe Met Asn Asp Pro Ala Met
      25                30                35

Asn Arg Gly Gly Ala
      40

```

(2) INFORMATION FOR SEQ ID NO: 360:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Hypertrophic prostate
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -18..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.7
 seq LPLLXXXSLPVGA/WL
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

Met Ala Arg His Gly Leu Pro Leu Leu Xaa Xaa Xaa Ser Leu Pro Val
 -15 -10 -5

Gly Ala Trp Leu
 1

(2) INFORMATION FOR SEQ ID NO: 361:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Cancerous prostate
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -37..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.7
 seq ILYLWYCSVCSS/GS
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

Met Val His Leu Arg Thr Gly Leu Met Leu Met Ser Ala Asp Arg Leu
 -35 -30 -25

Arg Thr Leu Tyr Tyr Thr Val Thr Ile Leu Tyr Ile Leu Trp Tyr Cys
 -20 -15 -10

Ser Val Cys Ser Ser Gly Ser Leu Leu Ser Thr Ser Ile Met Lys Lys
 -5 1 5 10

Arg Met

(2) INFORMATION FOR SEQ ID NO: 362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
 (B) LOCATION: -15..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.7
 seq ILSTVTALTFFARA/LD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

Met Gly Ile Leu Ser Thr Val Thr Ala Leu Thr Phe Ala Arg Ala Leu
-15 -10 -5 1

Asp Gly Cys Arg Asn Gly Ile Ala His Pro Ala Ser Glu Lys His Arg
5 10 15

Leu Glu Lys Cys Arg Glu Leu Glu Ser Ser His Ser Ala Pro Gly Ser
20 25 30

Thr Gln Gln
35

(2) INFORMATION FOR SEQ ID NO: 363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -23..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.5
seq LTFLQXLLLISSLX/RE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

```

Met Glu Leu Gly Cys Trp Thr Gln Leu Gly Leu Thr Phe Leu Gln Xaa
      -20              -15              -10
Leu Leu Ile Ser Ser Leu Xaa Arg Glu Tyr Thr Val Ile Asn Glu Ala
      -5              1              5
Arg Lys
10

```

(2) INFORMATION FOR SEQ ID NO: 364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -22...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.4
seq FLLCXSVFTDCKG/DV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

```

Met Glu Leu Leu Arg Val Cys Ser Phe Phe Leu Leu Cys Xaa Ser Val
      -20              -15              -10
Phe Thr Asp Cys Lys Gly Asp Val Leu Cys Val Lys Met Glu Gln Ser
      -5              1              5              10
Gln Ile Cys Ala

```

(2) INFORMATION FOR SEQ ID NO: 365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq TWFLLLPPGQCRA/VG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

Met Ile Val Arg Pro Arg Leu Asn Leu Thr Trp Phe Leu Leu Leu Pro
 -20 -15 -10

Pro Gly Gln Cys Arg Ala Val Gly Ala Thr Trp Pro Gly
 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq MVALCCCLWKISG/CE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

Met Gln Phe Leu Phe Lys Met Val Ala Leu Cys Cys Cys Leu Trp Lys
 -15 -10 -5

Ile Ser Gly Cys Glu Glu Val Pro Leu Thr Tyr Asn Leu Leu Lys Cys
 1 5 10

Leu Leu Asp Lys Ala His Val Gly
 15 20

(2) INFORMATION FOR SEQ ID NO: 367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -21..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.3
seq CVCAAAXXSQSLX/XX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

```

Met Leu Lys Val Ser Ala Val Leu Cys Val Cys Ala Ala Ala Xaa Xaa
-20                      -15                      -10

Ser Gln Ser Leu Xaa Xaa Xaa Ala Ala Val Ala Ala Ala Gly Gly Arg
-5                      1                      5                      10

Ser Asp Gly Gly Asn Phe Leu Asp Asp Lys Gln Trp Leu Thr Xaa Ile
15                      20                      25

Ser Gln Tyr Asp Lys Glu Xaa Gly Xaa Trp Asn Lys Phe Arg Asp Asp
30                      35                      40

Xaa Tyr
45

```

(2) INFORMATION FOR SEQ ID NO: 368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -21..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.3
seq MVALCCCLWKISG/CE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

```

Met Ser Met Gln Phe Leu Phe Lys Met Val Ala Leu Cys Cys Cys Leu
-20                      -15                      -10

Trp Lys Ile Ser Gly Cys Glu Glu Val Pro Leu Thr Tyr Asn Leu Leu
-5                      1                      5                      10

Lys Cys Leu Leu Asp Lys Ala His Cys Val Leu Leu Thr Pro Cys Gly

```

15

20

25

Tyr Ile Phe Ser Leu Ile Ser Pro Gly
30 35

(2) INFORMATION FOR SEQ ID NO: 369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.2
seq LWILLGSLSCRTS/NR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

Met Ala Gln His Leu Trp Ile Leu Leu Gly Ser Leu Ser Cys Arg Thr
-15 -10 -5

Ser Asn Arg Arg
1

(2) INFORMATION FOR SEQ ID NO: 370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.1
seq LYLFGFWTFXLG/KF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

Met Asn Lys Glu Xaa Val Ser Xaa Glu Arg Xaa Ala Gln Val Arg Leu
 -25 -20 -15

Tyr Leu Phe Ser Gly Phe Trp Thr Phe Xaa Leu Gly Lys Phe Lys Gln
 -10 -5 1

Gly Glu Xaa Ser Tyr Xaa Xaa Ile Leu Glu Arg Leu Leu Trp Gln Gln
 5 10 15 20

Gln Tyr Xaa Gly Trp Leu Val Gly Asp Lys Arg
 25 30

(2) INFORMATION FOR SEQ ID NO: 371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -54..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6
seq IVFIFLILLNTAA/QV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

Met Val Leu Trp Arg Ala Lys Ile Xaa Arg Asn Val Pro Val Thr Leu
 -50 -45 -40

Ser Glu Glu Asn Arg Ser Glu Gly Lys Val Gly Phe Gln Ala Tyr Lys
 -35 -30 -25

Asn Tyr Phe Arg Ala Gly Ala His Trp Ile Val Phe Ile Phe Leu Ile
 -20 -15 -10

Leu Leu Asn Thr Ala Ala Gln Val Ala Tyr Val Leu Gln Asp Trp Trp
 -5 1 5 10

Leu Ser Tyr Trp Ala Asn Lys Gln Ser Met Leu Asn Val Thr Val Asn
 15 20 25

(2) INFORMATION FOR SEQ ID NO: 372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -18..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 6
seq FTSVLWLTSPSQP/NT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

Met Leu Leu Xaa Phe Phe Thr Ser Val Leu Trp Leu Thr Ser Pro Ser
-15 -10 -5

Gln Pro Asn Thr Cys Pro Ser Ser Leu Leu Cys Thr Tyr Pro Asn Leu
1 5 10

Asn Pro Pro Trp
15

(2) INFORMATION FOR SEQ ID NO: 373:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -22..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.9
seq IILGCLALFLLQ/RK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

Met Glu Leu Ile Ser Pro Thr Val Ile Ile Ile Leu Gly Cys Leu Ala
-20 -15 -10

Leu Phe Leu Leu Leu Gln Arg Lys Asn Leu Arg Arg Pro Trp
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -47..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq TWLGLLSFQNLHC/FP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

Met His Gly Phe Glu Ile Ile Ser Leu Lys Glu Glu Ser Pro Leu Gly
-45 -40 -35
Lys Val Ser Gln Gly Pro Leu Phe Asn Val Thr Ser Gly Ser Ser Ser
-30 -25 -20
Pro Val Thr Trp Leu Gly Leu Leu Ser Phe Gln Asn Leu His Cys Phe
-15 -10 -5 1
Pro Asp Leu Pro Gly
5

(2) INFORMATION FOR SEQ ID NO: 375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -56..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq NTLFLHLSGLSAA/DT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

Met Thr Trp Val Arg His Ala Pro Gly Lys Ser Leu Glu Trp Val Ala
-55 -50 -45
Thr Val Thr Asp Gly Gly Asp Lys Thr Phe Tyr Ala Ala Ser Val Lys

-40 -35 -30 -25
Gly Arg Phe Asn Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe Leu
 -20 -15 -10
His Leu Ser Gly Leu Ser Ala Ala Asp Thr Gly Trp Trp Gly Ile
 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.8
seq LTSFFSLTANCQS/AG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

Met Leu Thr Ser Phe Phe Ser Leu Thr Ala Asn Cys Gln Ser Ala Gly
 -10 -5 1
Thr Ile Ser Phe Ala Ala Phe Ser Leu Met Pro Gly
 5 10

(2) INFORMATION FOR SEQ ID NO: 377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.8
seq LTPLFFMXPTGFS/SP

(xi). SEQUENCE DESCRIPTION: SEQ ID NO: 377:

Met Leu Leu Cys Leu Leu Thr Pro Leu Phe Phe Met Xaa Pro Thr Gly
-15 -10 -5
Phe Ser Ser Pro Ser Pro Gly
1 5

(2) INFORMATION FOR SEQ ID NO: 378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7
seq HSLFLSLLGLCPS/KT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

Met Asp Asp Asp Tyr Glu Ala Tyr His Ser Leu Phe Leu Ser Leu Leu
-20 -15 -10
Gly Leu Cys Pro Ser Lys Thr Pro Ile Asn Glu Asn Ala Pro Val Phe
-5 1 5 10
Asp Pro Glu Pro Val
15

(2) INFORMATION FOR SEQ ID NO: 379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.7
 seq WLVWLLLGHMVVS/QM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

Met Glu Trp Gly Lys Gln Trp Leu Val Trp Leu Leu Leu Gly His Met
 -15 -10 -5
 Val Val Ser Gln Met Ala Thr Leu Leu Ala Arg Lys His Arg Pro Trp
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 380:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -39..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.7
 seq LTQGVWLWILVIQA/VP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

Met Arg Arg Gly Lys Arg Leu Leu Glu Ser Gln Ser Ser Ser Pro Lys
 -35 -30 -25
 Ala Cys Leu Gln Leu Gly Phe Glu Thr Glu Leu Thr Gln Gly Val Leu
 -20 -15 -10
 Trp Ile Leu Val Ile Gln Ala Val Pro Val Pro Ser Leu Thr Lys Thr
 -5 1 5
 Lys
 10

(2) INFORMATION FOR SEQ ID NO: 381:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Normal prostate

- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -20..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.7
 seq ALLESVVWLPCHG/RG

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

Met Val Ala Ala Thr Glu Ala Ala Leu Leu Glu Ser Val Val Trp Leu
-20 -15 -10 -5

Pro Cys His Gly Arg Gly Gly Ser
 1

- (2) INFORMATION FOR SEQ ID NO: 382:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

- (ii) MOLECULE TYPE: PROTEIN

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Normal prostate

- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -19..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.6
 seq VSLPLLSSWGSTA/WT

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

Met Ser Trp Asn Pro Ser Val Ser Leu Pro Leu Leu Ser Ser Trp Gly
 -15 -10 -5

Ser Thr Ala Trp Thr Leu
 1

- (2) INFORMATION FOR SEQ ID NO: 383:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 47 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

- (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -22..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.6
seq LILLSLHLERRWT/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

```

Met Lys Arg Ile Gln Gly Ile Leu Phe Leu Ile Leu Leu Ser Leu His
-20                               -15                               -10

Leu Glu Arg Arg Trp Thr Ser Pro Ser Asp His Ser Leu Leu Leu Gly
-5                               1                               5                               10

Gly Asn Ser Leu Ala Gln His Ala Glu Ser Val Val Arg Gln Gly
15                               20                               25

```

(2) INFORMATION FOR SEQ ID NO: 384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -35..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.5
seq LLTFGLEVCLAAG/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

```

Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala
-35                               -30                               -25                               -20

Gln Leu Xaa Leu Xaa Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu
-15                               -10                               -5

Ala Ala Gly Ser Pro Met Cys Arg Leu Cys Cys Trp Lys Trp
1                               5                               10

```

(2) INFORMATION FOR SEQ ID NO: 385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq PFALVTSCSSVFS/GD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

```

Met Ala Ala Gly Val Pro Phe Ala Leu Val Thr Ser Cys Ser Ser Val
      -15              -10              -5
Phe Ser Gly Asp Gln Leu Val Gln His Ile Leu Gly Thr Glu Asp Leu
      1              5              10
Ile Val Glu Val Thr Ser Asn Asp Ala Val Arg Phe Tyr Pro Trp Thr
      15              20              25              30
Ile Asp Asn Lys Tyr Tyr Ser Ala Asp Ile Asn Leu Cys Val Val Pro
      35              40              45
Asn Lys Phe Leu Val Thr Ala Glu Ile Ala Glu Ser Val Gln Ala Phe
      50              55              60
Val Val Tyr Phe Asp Xaa Thr Gln Xaa Ser Gly Leu Asp Ser Val Ser
      65              70              75
Ser Trp Leu Pro Leu Ala Lys Ala Trp Leu Pro Glu Val Met Ile Leu
      80              85              90
Val Cys Asp Arg Val Ser Glu Asp Gly Ile
      95              100

```

(2) INFORMATION FOR SEQ ID NO: 386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq TVFLXFCFPRCHS/DS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

Met Thr Val Phe Leu Xaa Phe Cys Phe Pro Arg Cys His Ser Asp Ser
 -10 -5 1

His Xaa Xaa Gln Gln Ser Ala
 5

(2) INFORMATION FOR SEQ ID NO: 387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -48..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4
seq ILLEVFVWNGLOG/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

Met Xaa Pro Asn Asn Phe Trp Gln Lys Leu Gly Arg Lys Lys Pro Arg
 -45 -40 -35

Ile Phe Thr Cys Thr Gln Ser Ser Thr Gly Glu Ala Ala Val Lys Ala
 -30 -25 -20

Glu Asn Leu Ile Leu Leu Glu Val Phe Val Trp Asn Gly Leu Gln Gly
 -15 -10 -5

Leu Pro Ser Glu Leu Ser Asp Thr Ser Gly Ser Ser Lys Lys Leu Gly
 1 5 10 15

Ser Leu Val Gly Trp Trp Arg Thr Leu Lys Met Ala Pro Ala Cys Leu
 20 25 30

Trp Ser Met Trp Glu Ser Pro Pro Arg
 35 40

(2) INFORMATION FOR SEQ ID NO: 388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -36..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3
seq ALYIMCVPHSVWG/CA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

Met Phe Arg Ser Asp Arg Met Trp Xaa Cys His Trp Lys Trp Lys Pro
-35 -30 -25

Ser Pro Leu Leu Phe Leu Phe Ala Leu Tyr Ile Met Cys Val Pro His
-20 -15 -10 -5

Ser Val Trp Gly Cys Ala Asn Cys Arg Val Val Leu Ser Asn Pro Ser
1 5 10

Gly Thr Phe Thr Ser Pro Cys Tyr Pro Asn Asp Tyr Pro Asn Ser Gln
15 20 25

Ala Cys Met Trp Thr Leu Arg Asp Pro
30 35

(2) INFORMATION FOR SEQ ID NO: 389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3
seq LVALSSELPFLGA/GV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

Met Thr Gln Arg Ser Ile Ala Gly Pro Ile Cys Asn Leu Lys Phe Val
 -30 -25 -20

Thr Leu Leu Val Ala Leu Ser Ser Glu Leu Pro Phe Leu Gly Ala Gly
 -15 -10 -5 1

Val Gln Leu Gln Asp Asn Gly Tyr Asn Gly Leu Leu Ile Ala Ile Asn
 5 10 15

Pro Gln Val Pro Glu Asn Gln Asn Leu Ile Ser Asn Ile Lys Glu Met
 20 25 30

Ile Thr Glu Ala Ser Phe Tyr Leu Phe Asn Ala Thr Lys Arg Arg Val
 35 40 45

Phe Phe Arg Asn Ile Lys Ile Leu Ile Pro Ala Gln
 50 55 60

(2) INFORMATION FOR SEQ ID NO: 390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3
seq IIPLLLLRSACN/VH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

Met Ile Ile Pro Leu Leu Leu Leu Arg Ser Ala Cys Asn Val His
 -10 -5 1

Leu Pro His Gln Thr Ala Ser Pro Ala Ser Leu Ser Pro Gln Gly Leu
 5 10 15

Ala Trp Gly Leu Leu His Gly Gly Cys Ser Val Thr Val Arg
 20 25 30

(2) INFORMATION FOR SEQ ID NO: 391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -19..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.3
seq VLLLSXNLIQ/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

Met Xaa Ser Pro Leu Pro Val Leu Leu Leu Ser Xaa Asn Leu Asn Leu
-15 -10 -5

Ile Ile Gln Ser Ser
1

(2) INFORMATION FOR SEQ ID NO: 392:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -46..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.2
seq LLTFLVFTXKLSS/LN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

Met Leu Met Cys Lys Met Leu Lys Ser Gln Lys Asn Cys Gln Glu Asn
-45 -40 -35

Xaa Xaa Ile Lys Ile Ile Leu Phe Leu Lys Pro Met Cys Ser Pro Gln
-30 -25 -20 -15

Tyr Leu Leu Thr Phe Leu Val Phe Thr Xaa Lys Leu Ser Ser Leu Asn
-10 -5 1

Ile Xaa Lys Phe His
5

(2) INFORMATION FOR SEQ ID NO: 393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -52..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2
seq IIVILHCAASIIS/CP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

Met Lys Lys Lys Ser Ser Pro Asn Gln Tyr Leu His Ser Ser Leu His
-50 -45 -40

Xaa Ile Arg Leu Phe Ser Phe Leu His Phe Ser Glu Glu Gly Val Leu
-35 -30 -25

Leu Leu Ala Ile Asp Leu Lys Ile Ile Val Ile Leu His Cys Ala Ala
-20 -15 -10 -5

Ser Ile Ile Ser Cys Pro Ser
1

(2) INFORMATION FOR SEQ ID NO: 394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1
seq ATSVSLEAQSCFA/WP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

```

Met Phe Ser Cys Phe Phe Ser Thr Ser Leu Ala Thr Ser Val Ser Leu
      -20              -15              -10

Glu Ala Gln Ser Cys Phe Ala Trp Pro Leu Ile Val Ser Phe Pro Gln
      -5              1              5

Gly Ser Leu Leu Ser Pro Phe Leu Leu Met Ser Tyr Asn Leu Ser His
10              15              20              25

Leu Ile Tyr Ser Gly Glu Leu Asn Gly Arg Leu Tyr Ala Glu Asn Ser
      30              35              40

Gln Ile Cys Ile Cys Ser Pro Ala Gly
      45              50

```

(2) INFORMATION FOR SEQ ID NO: 395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -50..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1
seq RTALILAVCCGSA/SI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

```

Met His-His Gly Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys
-50              -45              -40              -35

Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala
      -30              -25              -20

Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly
      -15              -10              -5

Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser
      1              5              10

Ser Gln Asp Leu Ser Gly Gln Thr Ala Pro Gly
15              20              25

```

(2) INFORMATION FOR SEQ ID NO: 396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1
seq IYFFACFQALTSS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

Met Ser Pro Cys Ile Tyr Phe Phe Ala Cys Phe Gln Ala Leu Thr Ser
-15 -10 -5

Ser Ser Pro Pro Gln
1

(2) INFORMATION FOR SEQ ID NO: 397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1
seq VSGASGFLPPARS/RI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

Met Ala Glu Glu Met Glu Ser Ser Leu Glu Ala Xaa Phe Ser Ser Ser
-30 -25 -20

Gly Ala Val Ser Gly Ala Ser Gly Phe Leu Pro Pro Ala Arg Ser Arg
-15 -10 -5 1

Ile Phe Lys Ile Ile Val Ile Gly Asp Xaa Asn Val Gly Lys Thr Cys
5 10 15

Leu Thr Tyr Arg Phe Cys Ala Gly Arg Phe Pro Asp Arg Thr Glu Ala

20 25 30
 Thr Ile Gly Val Asp Phe Arg Glu Arg Ala Val Glu Ile Asp Gly Glu
 35 40 45
 Arg Ile Lys Ile Gln Leu Trp Asp Thr Ala
 50 55

(2) INFORMATION FOR SEQ ID NO: 398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1
seq VSGASGFLPPARS/RI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

Met Ala Glu Glu Met Glu Ser Ser Leu Glu Ala Ser Phe Ser Ser Ser
 -30 -25 -20
 Gly Ala Val Ser Gly Ala Ser Gly Phe Leu Pro Pro Ala Arg Ser Arg
 -15 -10 -5 1
 Ile Phe Lys Ile Ile Val Ile Gly Asp Ser Asn Val Xaa Lys Thr Cys
 5 10 15
 Leu Thr Tyr Arg Phe Cys Ala Gly Arg Phe Pro Asp Arg
 20 25 30

(2) INFORMATION FOR SEQ ID NO: 399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -27..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5
 seq HLSLILLKPLCLP/NN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

Met Leu Val Leu Gly Ser Pro Leu Leu Gly Pro Leu Leu Trp His Leu
 -25 -20 -15
 Ser Leu Ile Leu Leu Lys Pro Leu Cys Leu Pro Asn Asn Leu Pro Leu
 -10 -5 1 5
 Ala Leu Gly Arg Cys Leu Cys Leu His Ser
 10 15

(2) INFORMATION FOR SEQ ID NO: 400:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -55..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5
 seq VLFMTTAVDLVIT/EV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

Met His Leu Leu Asp Leu Glu Ser Met Gly Lys Ser Ser Asp Gly Lys
 -55 -50 -45 -40
 Ser Tyr Val Ile Thr Gly Ser Trp Asn Pro Lys Ser Pro His Phe Gln
 -35 -30 -25
 Val Val Asn Glu Glu Thr Pro Lys Asp Lys Val Leu Phe Met Thr Thr
 -20 -15 -10
 Ala Val Asp Leu Val Ile Thr Glu Val Gln Glu Pro Val Arg Phe Leu
 -5 1 5
 Leu Glu Thr Lys Val Arg Val Cys Ser Pro Asn Glu Arg Leu Phe Trp
 10 15 20 25
 Pro Ala

(2) INFORMATION FOR SEQ ID NO: 401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq VLFVFSSIIPLTFL/FQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

```

Met Glu Asn Leu Lys Asp Phe Tyr Val Leu Phe Val Phe Ser Ser Ile
  -20                -15                -10

Pro Leu Thr Phe Leu Phe Gln Lys Leu Pro Phe Val Trp Ile Xaa Glu
  -5                1                5                10

Glu Thr Leu Glu Thr Trp Tyr Leu Lys Ser Trp
      15                20

```

(2) INFORMATION FOR SEQ ID NO: 402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq LSIFSLVLPVCRM/HR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

```

Met Pro Gln Tyr Cys Leu Ser Ile Phe Ser Leu Val Leu Pro Val Cys
      -15                -10                -5

```

Arg Met His Arg
1

(2) INFORMATION FOR SEQ ID NO: 403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -43..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq LLAFGTSCSVVLY/DP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

Met	Val	Ala	Pro	Val	Leu	Glu	Thr	Ser	His	Val	Phe	Cys	Cys	Pro	Asn
			-40					-35					-30		
Arg	Val	Arg	Gly	Val	Leu	Asn	Trp	Ser	Ser	Gly	Pro	Arg	Gly	Leu	Leu
		-25				-20						-15			
Ala	Phe	Gly	Thr	Ser	Cys	Ser	Val	Val	Leu	Tyr	Asp	Pro	Leu	Gly	Cys
	-10				-5					1					5
Cys	Tyr	Gln	Leu	Glu	Trp	Ser	His	Arg	Pro	Phe	Arg				
			10					15							

(2) INFORMATION FOR SEQ ID NO: 404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -38..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq LSWLITWFGHXL/DF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

```

Met Pro Ile Ile Asp Gln Val Asn Pro Glu Leu His Asp Phe Met Gln
      -35                      -30                      -25

Ser Ala Glu Val Gly Thr Ile Phe Ala Leu Ser Trp Leu Ile Thr Trp
      -20                      -15                      -10

Phe Gly His Xaa Leu Ser Asp Phe Arg His Val Val Arg Leu Tyr Asp
      -5                      1                      5                      10

Phe Phe Leu Ala Cys His Pro Leu Met Pro Ile Tyr Phe Ala Ala Val
      15                      20                      25

Ile Val Leu Tyr Arg Glu Gln
      30

```

(2) INFORMATION FOR SEQ ID NO: 405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -49..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7
seq GLCVLVPCXSXX/WR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

```

Met Glu Thr Xaa Cys Pro Cys Cys Cys Cys Pro Cys Xaa Gly Xaa Gly
      -45                      -40                      -35

Ser Leu Xaa Xaa Lys Pro Val Tyr Glu Leu Gln Val Gln Lys Ser Val
      -30                      -25                      -20

Thr Val Gln Glu Gly Leu Cys Val Leu Val Pro Cys Ser Xaa Ser Xaa
      -15                      -10                      -5

Xaa Trp Arg Ser Trp Tyr Ser Ser Pro Pro Leu Tyr Val Tyr Trp Phe
      1                      5                      10                      15

Arg Asp Gly Glu Ile Pro Tyr Tyr Ala Glu Val Val Ala Thr Asn Asn
      20                      25                      30

Pro Asp Arg Arg Xaa Lys Xaa Xaa Xaa Xaa Xaa Pro Ile Pro Pro Pro
      35                      40                      45

```

Trp Gly Cys Pro Glu Glu Glu Leu
50 55

(2) INFORMATION FOR SEQ ID NO: 406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7
seq IYFFACFXXLTSS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

Met Ser Pro Cys Ile Tyr Phe Phe Ala Cys Phe Xaa Xaa Leu Thr Ser
-15 -10 -5

Ser Ser Pro Pro His Pro Cys Pro Lys Cys Trp Pro Ser Ser Gly Ser
1 5 10 15

Ile Pro Leu

(2) INFORMATION FOR SEQ ID NO: 407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7
seq VLKCLSFSXPSLP/GF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

Met Gly Arg Gly Glu Arg Arg His Tyr Trp Gly Pro Lys Leu Val Leu
 -25 -20 -15

Lys Cys Leu Ser Phe Ser Xaa Pro Ser Leu Pro Gly Phe Leu Trp Ser
 -10 -5 1 5

Leu

(2) INFORMATION FOR SEQ ID NO: 408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -52..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7
seq LLAKALHLLKSSC/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

Met Ser Gln Asp Gly Gly Xaa Gly Glu Leu Lys His Met Val Met Ser
 -50 -45 -40

Phe Arg Val Ser Glu Leu Gln Val Leu Leu Gly Phe Ala Gly Arg Asn
 -35 -30 -25

Lys Ser Gly Arg Lys His Glu Leu Leu Ala Lys Ala Leu His Leu Leu
 -20 -15 -10 -5

Lys Ser Ser Cys Ala Pro Ser Val Gln Met Lys Ile Lys Glu Leu Tyr
 1 5 10

Arg Arg Arg Phe Pro Arg Lys Thr Leu Gly Pro Ser Asp Leu Ser Leu
 15 20 25

Lys

(2) INFORMATION FOR SEQ ID NO: 409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -69..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.6
seq LGPSLSSLPSALS/LM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

```
Met His His Arg Met Asn Glu Met Asn Leu Ser Pro Val Gly Met Glu
                        -65                      -60                      -55
Gln Leu Thr Ser Ser Ser Val Ser Asn Ala Leu Pro Val Ser Gly Ser
                        -50                      -45                      -40
His Leu Gly Leu Ala Ala Ser Pro Thr His Ser Ala Ile Pro Ala Pro
                        -35                      -30                      -25
Gly Leu Pro Val Ala Ile Pro Asn Leu Gly Pro Ser Leu Ser Ser Leu
                        -20                      -15                      -10
Pro Ser Ala Leu Ser Leu Met Leu Pro Met Gly Xaa Gly Asp Arg Gly
                        -5                      1                      5                      10
Val Met Cys Gly Leu
                        15
```

(2) INFORMATION FOR SEQ ID NO: 410:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -19..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.6
seq IWNLFSLFSTSTT/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

```
Met Leu His Ser Asp Asn Ile Trp Asn Leu Phe Ser Leu Phe Ser Thr
                        -15                      -10                      -5
```


Ser Thr Thr Leu Pro Arg
1

(2) INFORMATION FOR SEQ ID NO: 411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq FHSAAGWSGGGQA/CG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

Met Gln Pro Ala Ser Pro Pro Ala Arg Trp Ser Phe His Ser Ala Ala
 -20 -15 -10

Gly Trp Ser Gly Gly Gly Gln Ala Cys Gly Gly His Ser Cys Asp Gln
 -5 1 5

Val Leu Ala Val Ile Glu Leu Leu Asn Pro Leu Arg
 10 15 20

(2) INFORMATION FOR SEQ ID NO: 412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5
seq LLAGSISHMFSQA/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

Met Cys Phe Ser Phe Leu Leu Ala Gly Ser Ile Ser His Met Phe Ser
-15 -10 -5
Gln Ala Leu Pro Leu His Ser Pro Gly Leu Pro Thr Thr Asn Arg Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO: 413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5
seq SILFHCSVCLFLC/QY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

Met Tyr Gly Phe Ile Ile Gly Leu Ser Ile Leu Phe His Cys Ser Val
-20 -15 -10
Cys Leu Phe Leu Cys Gln Tyr His Ala Trp
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5
seq SLLGCXLAININT/FP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

Met Ser Phe Gly Xaa Ile Leu Thr Phe Arg Val Ser Leu Leu Gly Cys
 -20 -15 -10

Xaa Leu Ala Ile Asn Ile Asn Thr Phe Pro
 -5 1

(2) INFORMATION FOR SEQ ID NO: 415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq LGRLCAGSSGVXG/AR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

Met Ala Val Tyr Val Gly Met Leu Arg Leu Gly Arg Leu Cys Ala Gly
 -20 -15 -10

Ser Ser Gly Val Xaa Gly Ala Arg Ala Xaa Leu Ser Arg Ser Trp Gln
 -5 1 5 10

Glu Ala Arg Leu Gln Gly Val Arg Phe Leu Ser Ser Arg Glu Val Asp
 15 20 25

Arg Met Val Ser Thr Pro Ile Gly Gly Leu Ser Tyr Val Gln Gly Cys
 30 35 40

Thr Lys Lys His Leu Asn Ser Lys Thr Val Gly Gln Cys Leu Glu Thr
 45 50 55

Thr Ala Gln Arg Val Pro
 60

(2) INFORMATION FOR SEQ ID NO: 416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Hypertrophic prostate

- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -23..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.4
 seq LVSIFFWEVTNA/FL

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

Met Phe Asn Thr Ile Tyr Leu Val Ile Ser Leu Val Ser Ile Phe Phe
 -20 -15 -10

Phe Trp Glu Val Thr Asn Ala Phe Leu Lys Ala Arg Arg Trp
 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 417:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -22..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.4
 seq SLPLTTGSSWSLS/SQ

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

Met Ala Leu Pro Pro Lys Gly Cys Gly Ser Leu Pro Leu Thr Thr Gly
 -20 -15 -10

Ser Ser Trp Ser Leu Ser Ser Gln Ile Gly Ser Pro Ala Ile Ser Asn
 -5 1 5 10

Pro Arg

(2) INFORMATION FOR SEQ ID NO: 418:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -16..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.3
seq FLSWASFLAPLLR/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

Met Phe Val Phe Leu Ser Trp Ala Ser Phe Leu Ala Pro Leu Leu Arg
-15 -10 -5

Ser Pro Phe Leu His Cys Leu Met Gly Met Pro Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 419:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -28..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.3
seq LLSCSPLXPLGKS/GF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

Met Xaa Met Lys Ser Ala Asn Lys Ile Thr Leu Leu Xaa His His Leu
-25 -20 -15

Leu Ser Cys Ser Pro Leu Xaa Pro Leu Gly Lys Ser Gly Phe Ser Ser
-10 -5 1

Cys Gln Arg Leu Gly Lys Arg Ala Leu Val Phe Pro Ile Xaa Lys Xaa
5 10 15 20

Ile Ile Thr

(2) INFORMATION FOR SEQ ID NO: 420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq SLLLLFIVIPQTP/RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

Met Cys Asn Tyr Asn Ile Tyr Val Leu Tyr Asn Ile Gly Tyr Leu Tyr
-30 -25 -20

His Pro Lys Ser Phe Leu Leu Leu Phe Ile Val Ile Pro Gln Thr Pro
-15 -10 -5

Arg Pro
1

(2) INFORMATION FOR SEQ ID NO: 421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq PLLAAPLLRSLLP/RX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

Met Ala Val Ala Met Val Lys Leu Cys Glu Arg Ala Gly Leu Pro Leu
-25 -20 -15

Leu Ala Ala Pro Leu Leu Arg Ser Leu Leu Pro Arg Xaa Pro Gln Pro
 -10 -5 1 5
 Gly Pro Ala Gln Pro Arg Ser Val Gln Gly Gln Arg Cys Pro Ala Arg
 10 15 20
 His Pro Pro Gly Asn Leu Val Cys Glu Arg Gly Ala Xaa Val Asn Gly
 25 30 35
 Val Thr Ala Gly Ala Xaa Gly Xaa Leu Arg Gly Leu His Arg Gly Xaa
 40 45 50
 Arg Ala Leu Gly Cys Ser Ala His Arg Pro Xaa His Ser Ala Arg Val
 55 60 65
 Arg Pro Pro Ala
 70

(2) INFORMATION FOR SEQ ID NO: 422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -122..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq DVLGLLKDVLLA/RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

Met Leu Asn Val Val Arg Ala Leu Arg Xaa Pro Gln Trp Cys Ala Glu
 -120 -115 -110
 Tyr Cys Leu Ser Ile His Tyr Gln His Gly Gly Val Ile Cys Thr Gln
 -105 -100 -95
 Val His Lys Gln Thr Val Val Gln Leu Ala Leu Arg Val Ala Asp Glu
 -90 -85 -80 -75
 Met Asp Val Asn Ile Gly His Glu Val Gly Tyr Val Ile Pro Phe Glu
 -70 -65 -60
 Asn Cys Cys Thr Asn Glu Thr Ile Leu Arg Tyr Cys Thr Asp Asp Met
 -55 -50 -45
 Leu Gln Arg Glu Met Met Ser Asn Pro Phe Leu Gly Ser Tyr Gly Val
 -40 -35 -30

Ile Ile Leu Asp Asp Ile His Glu Arg Ser Ile Ala Thr Asp Val Leu
-25 -20 -15
Leu Gly Leu Leu Lys Asp Val Leu Leu Ala Arg Pro Glu Leu Lys
-10 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq AGLCIGSTSYVHG/DI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

Met His Ala Gly Leu Glu Arg Xaa Ser Xaa Gln Lys Ala Leu Ala Gly
-25 -20 -15
Leu Cys Ile Gly Ser Thr Ser Tyr Val His Gly Asp Ile Leu Arg Thr
-10 -5 1 5
Glu Arg

(2) INFORMATION FOR SEQ ID NO: 424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -35..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq LLGSLSLWRWSAM/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:

Met Leu Asn Gly Pro Phe Gln His Arg Asn Ser Arg Ile Met Thr His
 -35 -30 -25 -20

Arg Ser Ala Glu Lys Thr Leu Leu Gly Ser Leu Ser Leu Trp Arg Trp
 -15 -10 -5

Ser Ala Met Glu Pro Thr Asp Arg Cys Thr Arg Val Gly
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -44..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq IAVGLTCQHVSHA/IS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

Met Arg Val Lys Asp Pro Thr Lys Ala Leu Pro Glu Lys Ala Lys Arg
 -40 -35 -30

Ser Lys Arg Pro Thr Val Pro His Asp Glu Asp Ser Ser Asp Asp Ile
 -25 -20 -15

Ala Val Gly Leu Thr Cys Gln His Val Ser His Ala Ile Ser Val Asn
 -10 -5 1

His Val Lys Arg Ala Ile Ala Glu Asn Leu Trp Ser Val Cys Ser Glu
 5 10 15 20

Cys Leu Lys Glu Arg Arg Phe Tyr Asp Gly Gln Leu Val Leu Thr Ser
 25 30 35

Asp Ile Trp Leu Cys Leu Lys Cys Gly Phe Gln Gly Cys Gly Lys Asn
 40 45 50

Ser Glu Ser Gln His Ser Leu Lys His Phe Lys Ser Ser Arg Thr Glu
 55 60 65

Pro His Cys Ile Ile Ile Asn Leu Ser Thr
 70 75

(2) INFORMATION FOR SEQ ID NO: 426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -28..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4
seq FSLIALSMLKGTG/KV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

Met Pro Gln Lys Gly Leu Gly Leu Leu Gly Ile Leu Ser Gly Asp Phe
-25 -20 -15

Ser Leu Leu Ala Leu Ser Met Leu Lys Gly Thr Gly Lys Val Gly Gly
-10 -5 1

(2) INFORMATION FOR SEQ ID NO: 427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -55..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4
seq AALCGISLSQLFP/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

Met Ala Met Trp Asn Arg Pro Xaa Xaa Xaa Leu Pro Gln Gln Pro Leu
-55 -50 -45 -40

Xaa Ala Glu Pro Thr Ala Glu Gly Glu Pro His Leu Pro Thr Gly Arg
-35 -30 -25

Xaa Xaa Thr Glu Ala Asn Arg Phe Ala Tyr Ala Ala Leu Cys Gly Ile
 -20 -15 -10
 Ser Leu Ser Gln Leu Phe Pro Glu Pro Glu His Ser Ser Phe Cys Thr
 -5 1 5
 Glu Phe Met Ala Gly Leu Val Xaa Trp Leu Glu Leu Ser Glu Ala Val
 10 15 20 25
 Leu Pro Thr Met Thr Ala
 30

(2) INFORMATION FOR SEQ ID NO: 428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq LLLSPWVTVPVWS/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

Met Leu Cys Phe Gly Asp Leu Leu Leu Ser Pro Trp Val Thr Val Pro
 -15 -10 -5
 Val Trp Ser Ser Ser Pro Trp
 1

(2) INFORMATION FOR SEQ ID NO: 429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide

(B) LOCATION: -27..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4
 seq LIYFLGLAADTYF/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

```

Met Gln Glu Asn Ala His Asn Leu Arg Leu Phe Lys Cys Leu Leu Ile
  -25                      -20                      -15

Tyr Phe Leu Gly Leu Ala Ala Asp Thr Tyr Phe Arg Ser Lys Arg Lys
  -10                      -5                      1                      5

Pro Val Ser Phe Val Val Thr Val Xaa Xaa Gly Xaa Tyr Ala Thr Gly
          10                      15                      20
  
```

(2) INFORMATION FOR SEQ ID NO: 430:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 63 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -59..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4
 seq SVATALFPPLCIS/TG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

```

Met His Thr Cys Ser Leu Pro Cys Leu Leu Phe Ala Gln Leu Leu Glu
      -55                      -50                      -45

Phe Cys Ser Phe Pro Pro Asp Val Pro His Asn Cys Ala Pro Ile Val
      -40                      -35                      -30

Ser Val Arg Pro Pro Asn Ile Val Ala Ala Phe Glu Gly Cys Ser Val
      -25                      -20                      -15

Ala Thr Ala Leu Phe Pro Pro Leu Cys Ile Ser Thr Gly Asn Glu
      -10                      -5                      1
  
```

(2) INFORMATION FOR SEQ ID NO: 431:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 96 amino acids
 (B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -28..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4
seq PLLGVLFQGVYI/VF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

```
Met Gln Gln Arg Gly Ala Ala Gly Ser Arg Gly Cys Ala Leu Phe Pro
      -25                      -20                      -15

Leu Leu Gly Val Leu Phe Phe Gln Gly Val Tyr Ile Val Phe Ser Leu
      -10                      -5                      1

Glu Ile Arg Ala Asp Ala His Val Arg Gly Tyr Val Gly Glu Lys Ile
      5                      10                      15                      20

Lys Leu Lys Cys Thr Phe Lys Ser Thr Ser Asp Val Thr Asp Lys Leu
      25                      30                      35

Thr Ile Asp Trp Thr Tyr Arg Pro Pro Ser Ser Ser His Thr Val Ser
      40                      45                      50

Ile Xaa His Tyr Gln Ser Phe Gln Tyr Pro Thr Thr Ala Gly Thr Phe
      55                      60                      65
```

(2) INFORMATION FOR SEQ ID NO: 432:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -39..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.9
seq LILNRS LPTASSS/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:

```

Met Ala Phe Asp Val Ser Cys Phe Phe Trp Val Val Leu Phe Ser Ala
-20              -15              -10              -5

Gly Cys Lys Val Ile Thr Ser Trp Asp Gln Met Tyr Ile Glu Lys Glu
              1              5              10

Ala Asn Lys Thr Tyr Asn Cys Glu Asn Leu Gly Leu Ser Glu Ile Pro
              15              20              25

Asp Thr Leu Pro Asn Thr Thr Glu Phe Leu Glu Phe Ser Phe Asn Phe
              30              35              40

Leu Pro Thr Ile His Asn Arg Thr Ser Ser Arg
45              50              55

```

(2) INFORMATION FOR SEQ ID NO: 434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -96..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq IMNLTVMLDTAXG/KX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

```

Met Glu Val Ala Ala Asn Cys Ser Leu Arg Val Lys Arg Pro Leu Leu
-95                      -90                      -85

Asp Pro Arg Phe Glu Gly Tyr Lys Xaa Ser Leu Glu Pro Leu Pro Cys
-80                      -75                      -70                      -65

Tyr Gln Leu Glu Leu Asp Ala Ala Val Ala Xaa Val Lys Leu Arg Asp
                      -60                      -55                      -50

Asp Gln Tyr Thr Leu Glu His Met His Ala Phe Gly Met Tyr Asn Tyr
                      -45                      -40                      -35

Leu His Cys Asp Ser Trp Tyr Gln Asp Ser Val Tyr Tyr Ile Asp Thr
                      -30                      -25                      -20

Leu Gly Arg Ile Met Asn Leu Thr Val Met Leu Asp Thr Ala Xaa Gly
-15                      -10                      -5

Lys Xaa Arg Glu Val Phe Arg Leu Leu
 1                      5

```

(2) INFORMATION FOR SEQ ID NO: 435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -39..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq VLAIGLLHIVLLS/IP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

```

Met Asn Val Gly Thr Ala His Xaa Xaa Val Asn Pro Asn Thr Arg Val
      -35                      -30                      -25

Met Asn Ser Arg Gly Ile Trp Leu Ser Tyr Val Leu Ala Ile Gly Leu
      -20                      -15                      -10

Leu His Ile Val Leu Leu Ser Ile Pro Phe Val Ser Val Pro Val Val
      -5                      1                      5

Trp Thr Leu Thr Asn Leu Ile His Asn Met Gly Met Tyr Ile Phe Leu
      10                      15                      20                      25

His Thr Val Lys Gly Xaa Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala
      30                      35                      40

Arg Leu Leu Xaa His Xaa Xaa Ala Asp Gly Leu Trp Gly Pro Val
      45                      50                      55

```

(2) INFORMATION FOR SEQ ID NO: 436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq SWWTLLSSSPSFM/IS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

```

Met Glu Asn Phe Asn Met Tyr Lys Asn Lys Ser Trp Trp Thr Leu Leu
      -20                      -15                      -10

Ser Ser Ser Pro Ser Phe Met Ile Ser Phe Val Ser Ser Val Leu Pro
      -5                      1                      5

Val Leu Leu Thr Ile Ser Arg Phe Ile Leu Lys Gln Ile Pro Asp Gln
      10                      15                      20                      25

```


(2) INFORMATION FOR SEQ ID NO: 437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -39..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq VLAIGLLHIVLLS/IP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

Met Asn Val Gly Thr Xaa His Ser Glu Val Asn Pro Asn Thr Arg Val
 -35 -30 -25

Met Asn Ser Arg Gly Ile Trp Leu Ser Tyr Val Leu Ala Ile Gly Leu
 -20 -15 -10

Leu His Ile Val Leu Leu Ser Ile Pro Phe Val Ser Val Pro Val Val
 -5 1 5

Trp Thr Leu Thr Asn Leu Ile His Asn Met Gly Met Tyr Ile Phe Leu
10 15 20 25

Tyr Thr Val Lys Gly Thr
 30

(2) INFORMATION FOR SEQ ID NO: 438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8

seq AAASAVSVLLVAA/ER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

Met Ala Ala Ala Ser Ala Val Ser Val Leu Leu Val Ala Ala Glu Arg
 -10 -5 1

Asn Arg Trp His Arg Leu Pro Ser Leu Leu Leu Pro Pro Arg Thr Trp
 5 10 15

Val Trp Arg Gln Arg Thr Met Lys Tyr Thr Thr Ala Thr Gly Arg Asn
 20 25 30

Met
 35

(2) INFORMATION FOR SEQ ID NO: 439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -44..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
 seq SGSGLSWARLSQS/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

Met Ala Tyr Ser Lys Ala Ser Gly Ser Pro Val Leu Ser Gln Ala Val
 -40 -35 -30

Pro Gly Glu Asn Ala Ser His Arg Arg Gly Ser Ala Asp Leu Gly Ser
 -25 -20 -15

Gly Ser Gly Leu Ser Trp Ala Arg Leu Ser Gln Ser Arg Ser Glu Ile
 -10 -5 1

His Ser Ala Gly Pro Pro His Leu Gly Gly Arg Thr Asn Gly Pro Glu
 5 10 15 20

Phe Pro Ala Leu Ser Tyr Ser Ser Gln Leu Leu Ser Leu Ala Gln Leu
 25 30 35

Arg Gly Arg Gly Ile Thr Glu Val Ser Glu Lys Ser Pro Leu Ile
 40 45 50

(2) INFORMATION FOR SEQ ID NO: 440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -37..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq RPVLLHLHQTAHA/DE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:

Met Lys Pro Arg Arg Asn Leu Glu Glu Asp Asp Tyr Leu His Lys Asp
-35 -30 -25

Thr Gly Glu Thr Ser Met Leu Lys Arg Pro Val Leu Leu His Leu His
-20 -15 -10

Gln Thr Ala His Ala Asp Glu Phe Asp Cys Pro Ser Glu Leu Gln His
-5 1 5 10

Thr Gln Glu Leu Phe Pro Gln Trp His Leu Pro Ile Lys Ile Ala Ala
15 20 25

Ile Ile Ala Ser Leu Thr Phe Leu Tyr Thr Leu Leu Arg Glu Val Ile
30 35 40

His Pro Leu Ala Thr Ser His Gln Gln Tyr Phe Tyr Lys Ile Gln
45 50 55

(2) INFORMATION FOR SEQ ID NO: 441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.7
seq IPCAHLVCPTIG/DI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441:

```

Met Ile Ile Cys Tyr Asp Ile Pro Cys Ala His Met Leu Val Cys Pro
      -15                      -10                      -5
Thr Ile Gly Asp Ile Lys Phe Asp His Leu Met Lys Trp Tyr Pro Ser
      1                      5                      10
Asp Phe Ser Thr Glu Arg Leu
      15                      20

```

(2) INFORMATION FOR SEQ ID NO: 442:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -19..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq STLASVPPAATFG/AD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442:

```

Met Tyr Ser Ser Glu Asp Ser Thr Leu Ala Ser Val Pro Pro Ala Ala
      -15                      -10                      -5
Thr Phe Gly Ala Asp Asp Leu Val Leu Thr Leu Ser Asn Pro Gln Met
      1                      5                      10
Ser Leu Glu Gly Thr Glu Lys Ala Ser Trp Leu Gly Glu Gln Pro Gln
      15                      20                      25
Phe Trp Ser Lys Thr Gln Val Leu Asp Trp Ile Ser Tyr Gln Val Glu
      30                      35                      40                      45
Lys Asn Lys Tyr Asp Ala
      50

```

(2) INFORMATION FOR SEQ ID NO: 443:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -65..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7
seq QLEGLNWLRFSA/QG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443:

```

Met Gly Glu Asp Pro Xaa Gln Pro Arg Lys Tyr Lys Lys Xaa Lys Xaa
-65                               -60                               -55                               -50

Glu Leu Gln Gly Asp Xaa Pro Pro Ser Ser Pro Thr Asn Asp Pro Thr
                               -45                               -40                               -35

Val Lys Tyr Glu Thr Gln Pro Arg Phe Ile Thr Ala Thr Gly Gly Thr
                               -30                               -25                               -20

Leu His Met Tyr Gln Leu Glu Gly Leu Asn Trp Leu Arg Phe Ser Trp
                               -15                               -10                               -5

Ala Gln Gly Thr Xaa Gly
  1                               5

```

(2) INFORMATION FOR SEQ ID NO: 444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -42..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7
seq LLGCLQCCWLQSG/RA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:

```

Met Phe Tyr Val Ala Met Thr Lys Thr His Lys Arg Ile Arg Ser Leu
-40                               -35                               -30

```

Cys Asn Ile His His Gly Leu Phe Gln Phe Thr Gln Gln Leu Leu Gly
 -25 -20 -15

Cys Leu Gln Cys Cys Trp Leu Gln Ser Gly Arg Ala Pro Ala Thr Tyr
 -10 -5 1 5

Tyr Leu Val Glu Ser Ile Glu Lys Ser Ala His Gly Ser Val Leu Xaa
 10 15 20

Thr Tyr Asp Gln Thr Gln Thr Arg Ile Gly Arg
 25 30

(2) INFORMATION FOR SEQ ID NO: 445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -60...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7
seq XTCASXNPSQCLA/AF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445:

Met Val Ser Pro Lys Asp Leu Pro Leu Val Leu Leu Gln Asp Ile Lys
 -60 -55 -50 -45

Val Pro Ser Ser Met Thr Gly Ser His Ala Gly Asn Pro His Ile Glu
 -40 -35 -30

Arg Asn Asp Leu Pro Arg His Gly Ser Pro Gln Phe Phe Thr Gly Xaa
 -25 -20 -15

Thr Cys Ala Ser Xaa Asn Pro Ser Gln Cys Leu Ala Ala Phe
 -10 -5 1

(2) INFORMATION FOR SEQ ID NO: 446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -15..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.6
seq FXSLFCLYFSCFL/HI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

Met Glu Phe Xaa Ser Leu Phe Cys Leu Tyr Phe Ser Cys Phe Leu His
-15 -10 -5 1

Ile Ile Tyr Phe Xaa Ser Cys Phe Leu Tyr
5 10

(2) INFORMATION FOR SEQ ID NO: 447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -45..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.6
seq ALLELIDSPECLS/KC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

Met Ala Leu His Phe Gln Ser Leu Ala Glu Leu Glu Xaa Leu Cys Thr
-45 -40 -35 -30

His Leu Tyr Ile Gly Thr Asp Leu Thr Gln Arg Ile Glu Ala Glu Lys
-25 -20 -15

Ala Leu Leu Glu Leu Ile Asp Ser Pro Glu Cys Leu Ser Lys Cys Gln
-10 -5 1

Leu Leu Leu Glu Gln Gly Thr Thr Ser Tyr Ala Gln Leu Leu Ala Ala
5 10 15

Thr Xaa
20

(2) INFORMATION FOR SEQ ID NO: 448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq LLLLLITPSPSPL/LF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448:

Met Arg Thr Leu Phe Gly Ala Val Arg Ala Pro Phe Ser Ser Leu Thr
-25 -20 -15

Leu Leu Leu Ile Thr Pro Ser Pro Ser Pro Leu Leu Phe Asp Arg Gly
-10 -5 1 5

Leu Ser Leu Arg Ser Ala Met Ser
10

(2) INFORMATION FOR SEQ ID NO: 449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -41..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq AVSSLIAVGTSHG/LA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449:

Met Arg His Ser Leu Leu Lys Gly Ile Ser Ala Gln Ile Val Ser Ala
-40 -35 -30

Ala Asp Lys Val Asp Ala Gly Leu Pro Thr Ala Ile Ala Val Ser Ser
-25 -20 -15 -10

Leu Ile Ala Val Gly Thr Ser His Gly Leu Ala Gly
 * -5 1

(2) INFORMATION FOR SEQ ID NO: 450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq LSCFIFFYISSLC/CF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450:

Met Thr Leu Ser Cys Phe Ile Phe Phe Tyr Ile Ser Ser Leu Cys Cys
-15 -10 -5 1

Phe Leu Ser Tyr Pro Thr Arg
 5

(2) INFORMATION FOR SEQ ID NO: 451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq LCFLLP HHRLQEA/RQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451:

Met Ile Leu Cys Phe Leu Leu Pro His His Arg Leu Gln Glu Ala Arg
-15 -10 -5 1
Gln Ile Gln Val Leu Lys Met Leu Pro Arg Glu Lys Leu Arg Arg Arg
5 10 15
Arg Arg Glu Lys Thr Asn Lys Trp Glu Lys Arg Lys Gly Ser Gly
20 25 30

(2) INFORMATION FOR SEQ ID NO: 452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq FSLFALNMPLGFC/VY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452:

Met Phe Ser Leu Phe Ala Leu Asn Met Pro Leu Gly Phe Cys Val Tyr
-10 -5 1
Val Ile Phe Lys Ile His Asp Trp
5 10

(2) INFORMATION FOR SEQ ID NO: 453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5

seq SVWGVLPFPACSA/DL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453:

```

Met Ala Ser Ser Pro Gly Val Ala Met His Ser Leu Trp Ala Thr Ile
  -30                -25                -20

His Thr Ser Val Trp Gly Val Leu Pro Pro Pro Ala Cys Ser Ala Asp
-15                -10                -5                1

Leu Leu Phe Ser Asn Ala Cys Leu Leu Pro His Glu Ile His Leu
      5                10                15

```

(2) INFORMATION FOR SEQ ID NO: 454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -45...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq LPRLLSLSQHSSES/WI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 454:

```

Met Ser Gln Glu Gly Ala Val Pro Ala Ser Ala Val Pro Leu Glu Glu
-45                -40                -35                -30

Leu Ser Ser Trp Pro Glu Glu Leu Cys Arg Arg Glu Leu Pro Ser Val
      -25                -20                -15

Leu Pro Arg Leu Leu Ser Leu Ser Gln His Ser Glu Ser Trp Ile Glu
      -10                -5                1

His Ile Gln Ile Leu Lys Ile Ile Val Glu Met Phe Leu Pro His Met
      5                10                15

Asn His Leu Thr Leu Glu Gln Thr Phe Phe Ser Gln Val Leu Pro Lys
20                25                30                35

Thr Val Lys Leu Phe Asp
      40

```

(2) INFORMATION FOR SEQ ID NO: 455:

Ile Ala Asp Cys Ala Tyr Arg Asp Leu Glu Ser Val Pro Pro Gly Phe
 15 20 25 30
 Pro Ala Asn Val Thr Thr Leu Ser Leu Ser Ala Asn Arg Leu Pro Gly
 35 40 45
 Leu Pro Glu Gly Ala Phe Arg Glu Val Pro Leu Leu Gln Ser Leu Trp
 50 55 60
 Leu Ala His Asn Glu
 65

(2) INFORMATION FOR SEQ ID NO: 457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 13.6
seq LLLALCATGAQG/LY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 457:

Met Gly Arg Gln Ala Leu Leu Leu Leu Ala Leu Cys Ala Thr Gly Ala
 -15 -10 -5
 Gln Gly Leu Tyr Phe His Ile Gly Glu Thr Glu Lys Arg Cys Phe Ile
 1 5 10
 Glu Glu Ile Pro Asp Glu Thr Met Val Ile Gly Asn Tyr Arg Thr Gln
 15 20 25 30
 Met Trp Asp Lys Gln Lys Glu Val Phe Leu Pro Ser Thr Pro Gly Leu
 35 40 45
 Gly Met His Val Glu Val Lys Asp Pro Asp Gly Lys Val Val Leu Ser
 50 55 60
 Arg Gln Tyr Gly Ser Glu Gly Arg Phe Thr Phe Thr Ser His Xaa Xaa
 65 70 75
 Gly Asp His Gln Ile Cys Leu His Cys Gly
 80 85

(2) INFORMATION FOR SEQ ID NO: 458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -21..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 12.7
seq ILFLLSWSGPLQG/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 458:

Met Gly Pro Ser Thr Pro Leu Leu Ile Leu Phe Leu Leu Ser Trp Ser
-20 -15 -10

Gly Pro Leu Gln Gly Gln Gln His His Leu Val Glu Tyr Met Glu Arg
-5 1 5 10

Arg Leu Ala Ala Leu Glu Glu Arg
15

(2) INFORMATION FOR SEQ ID NO: 459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -27..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.8
seq LLLLCPLSRGCCP/LL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459:

Met Ser Cys Arg Glu Leu Thr His Arg Pro Cys Ser Pro His Leu Leu
-25 -20 -15

Leu Leu Cys Pro Leu Ser Arg Gly Cys Cys Pro Leu Leu Leu Ser Xaa
-10 -5 1 5

Pro Leu Xaa Gly Val Asn Leu Glu Ser Ile Leu Ser Leu Thr Leu Pro
 10 15 20

Pro Ser Pro Ser Ser Val Gly Leu Ser Pro Ser Val Thr Xaa Leu Thr
 25 30 35

Thr Ser Pro Val Ser Leu His Phe Ala Ser Xaa Leu Ala Gly
 40 45 50

(2) INFORMATION FOR SEQ ID NO: 460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.5
seq AALLLGLMMVVTG/DE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 460:

Met Gly Trp Thr Met Arg Leu Val Thr Ala Ala Leu Leu Leu Gly Leu
 -20 -15 -10

Met Met Val Val Thr Gly Asp Glu Asp Glu Asn Ser Pro Cys Ala His
 -5 1 5 10

Glu Ala Leu Leu Asp Glu Asp Thr Leu Phe Cys Gln Gly Leu Glu Val
 15 20 25

Phe Tyr Pro Glu Leu Gly Asn Ile Gly Cys Lys Val Val Pro Asp Cys
 30 35 40

Xaa Asn Tyr Arg Gln Lys Ile Thr Ser Trp Met Glu Pro Ile Val Lys
 45 50 55

Phe Pro Gly Ala Val Asp Gly Ala Thr Tyr Ile Leu Val Met Val Asp
 60 65 70

Pro Asp Ala Pro Ser Arg Ala Glu Pro Arg Gln Arg Phe Trp Arg His
 75 80 85 90

Trp Leu Val Thr Asp Ile Lys Gly Ala
 95

(2) INFORMATION FOR SEQ ID NO: 461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.3
seq VHLLSLCSGKVYA/RM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461:

Met Lys Phe Leu Ile Phe Ala Phe Phe Gly Gly Val His Leu Leu Ser
-20 -15 -10

Leu Cys Ser Gly Lys Val Tyr Ala Arg Met Ala Ser Leu Arg Gly Leu
-5 1 5

Gly

(2) INFORMATION FOR SEQ ID NO: 462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.1
seq LIFLCGAALLAVG/IW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462:

Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu
-25 -20 -15

Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val
-10 -5 1

Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser
 5 10 15

Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly
 20 25 30 35

Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr
 40 45 50

Glu Ser Lys Cys Ala Leu Val Thr Phe
 55 60

(2) INFORMATION FOR SEQ ID NO: 463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.6
seq IVSLLGFVATVTL/IP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463:

Met Trp Ala Phe Ser Glu Leu Pro Met Pro Leu Leu Ile Asn Leu Ile
 -25 -20 -15

Val Ser Leu Leu Gly Phe Val Ala Thr Val Thr Leu Ile Pro Ala Phe
 -10 -5 1

Arg Gly His Phe Ile Ala Ala Arg Leu Cys Gly Gln Asp Leu Asn Lys
 5 10 15 20

Thr Ser Gln

(2) INFORMATION FOR SEQ ID NO: 464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -19..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.3
seq VLMRLVASAYSIA/QK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464:

Met Ala Ser Ser Asn Thr Val Leu Met Arg Leu Val Ala Ser Ala Tyr
 -15 -10 -5

Ser Ile Ala Gln Lys Ala Gly Met Ile Val Arg Arg Val Ile Ala Glu
 1 5 10

Gly Asp Leu Gly Ile Val Glu Xaa Thr Cys Ala Thr Asp Leu Gln Thr
 15 20 25

Lys Ala Asp Arg Leu Ala Gln Met Xaa Ile Cys Ser Ser Leu Ala Arg
 30 35 40 45

Lys Phe Pro Lys Leu Thr Ile Ile Gly Glu Glu Asp Leu Pro Ser Xaa
 50 55 60

Glu Val Asp Gln Glu
 65

(2) INFORMATION FOR SEQ ID NO: 465:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -24..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.9
seq VHLLSLCSGKAIC/KN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465:

Met Lys Phe Leu Ile Phe Ala Phe Phe Gly Gly Val His Leu Leu Ser
 -20 -15 -10

Leu Cys Ser Gly Lys Ala Ile Cys Lys Asn Gly Ile Ser Lys Arg Thr
 -5 1 5

Phe Glu Glu Ile Lys Glu Glu Ile Ala Ser Cys Gly Asp Val Ala Lys
 10 15 20
 Ala Ile Ile Asn Leu Ala Val Tyr Gly Lys Ala Gln Asn Arg Ser Tyr
 25 30 35 40
 Xaa Arg Leu Ala Leu Leu Val
 45

(2) INFORMATION FOR SEQ ID NO: 466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -51..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq ALXVLPLLGLHEA/AS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466:

Met Ala Asp Thr Thr Pro Asn Gly Pro Gln Gly Ala Gly Ala Val Gln
 -50 -45 -40
 Phe Met Met Thr Asn Lys Leu Asp Thr Ala Met Trp Leu Ser Arg Leu
 -35 -30 -25 -20
 Phe Thr Val Tyr Cys Ser Ala Leu Xaa Val Leu Pro Leu Leu Gly Leu
 -15 -10 -5
 His Glu Ala Ala Ser Phe Tyr Gln Arg Ala Leu Leu Ala Asn Ala Leu
 1 5 10
 Thr Ser Ala Leu Arg Leu His Gln Arg Leu Pro His Phe Gln Leu Ser
 15 20 25
 Arg Ala Phe Leu Ala Gln Ala Leu Leu Glu Asp Ser Cys His Tyr Leu
 30 35 40 45
 Leu Tyr Ser Leu Ile Phe Val Asn Ser Tyr Pro Val Thr Met Ser Ile
 50 55 60
 Phe Pro Val Leu Leu Phe
 65

(2) INFORMATION FOR SEQ ID NO: 467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq XVLVLSVVXXAMA/AF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467:

Met Arg Phe Arg His Phe Xaa Lys Xaa Ile Gly Xaa Val Leu Val Leu
 -20 -15 -10

Ser Val Val Xaa Xaa Ala Met Ala Ala Phe Ala Val Xaa Pro Gln Gly
 -5 1 5

Pro Ala Leu Xaa Ser Glu Pro Xaa Xaa Xaa Gly Ser Pro Thr Ser Pro
 10 15 20

Lys Pro Gly Val Asn Ala Gln Phe Leu Pro Gly Phe Leu Met Gly Xaa
 25 30 35 40

Leu Pro Ala Pro Val Thr Pro Gln Pro
 45

(2) INFORMATION FOR SEQ ID NO: 468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -40..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2
seq LCVEFASVASCDA/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 468:

```

Met Glu Leu Gly Ser Cys Leu Glu Gly Gly Arg Glu Ala Ala Glu Glu
-40                -35                -30                -25

Glu Gly Glu Pro Glu Val Lys Lys Arg Arg Leu Leu Cys Val Glu Phe
                -20                -15                -10

Ala Ser Val Ala Ser Cys Asp Ala Ala Val Ala Gln Cys Phe Leu Ala
                -5                1                5

Glu Asn Asp Trp Glu Met Glu Arg Ala Leu Asn Ser Tyr Phe Glu Pro
10                15                20

Pro Val Glu Glu Ser Ala Leu Glu Arg Arg Pro Glu Thr Ile Ser Glu
25                30                35                40

Pro Lys Thr Tyr Val Asp Leu Thr Asn Glu Glu Thr Thr Asp Ser Thr
                45                50                55

Thr Ser Lys Ile Ser Pro Ser Glu Asp Thr Gln Gln Glu Asn Gly Ser
                60                65                70

Met Phe Ser Leu Ile Thr Trp Asn Ile Asp Gly Leu Asp Leu Asn Asn
                75                80                85

Leu Ser Glu Arg Ala Arg Gly Val Cys Ser Tyr Leu Ala Leu Tyr Ser
90                95                100

Pro Asp Val Ile Phe Leu Gln Glu Val Ile Pro Pro Tyr Tyr Ser Tyr
105                110                115                120

Leu

```

(2) INFORMATION FOR SEQ ID NO: 469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -122..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq RLVVVSVPQSRA/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469:

```

Met Ala Ser Pro Phe Ser Gly Ala Leu Gln Leu Thr Asp Leu Asp Asp
-120                -115                -110

```

```

Phe Ile Gly Pro Ser Gln Glu Cys Ile Lys Pro Val Lys Val Glu Lys
-105                      -100                      -95

Arg Ala Gly Ser Gly Val Ala Lys Ile Arg Ile Glu Asp Asp Gly Ser
-90                      -85                      -80                      -75

Tyr Phe Gln Ile Asn Gln Asp Gly Xaa Thr Arg Arg Leu Glu Lys Ala
                      -70                      -65                      -60

Lys Val Ser Leu Asn Tyr Cys Xaa Ala Cys Ser Gly Cys Ile Thr Ser
                      -55                      -50                      -45

Ala Glu Thr Val Leu Ile Thr Gln Gln Ser His Glu Glu Leu Lys Lys
                      -40                      -35                      -30

Val Leu Asp Ala Asn Lys Met Ala Ala Pro Ser Gln Gln Arg Leu Val
-25                      -20                      -15

Val Val Ser Val Ser Pro Gln Ser Arg Ala Ser Leu Ala Ala Arg Phe
-10                      -5                      1                      5

Gln Leu Xaa Pro Thr Asp Thr Ala Arg Lys Leu Thr Ser Phe Phe Lys
                      10                      15                      20

```

(2) INFORMATION FOR SEQ ID NO: 470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -44..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq SLVAELLGAGSG/SH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470:

```

Met Gly Pro Val Pro Thr Ala Val Ala Gly Ala Gly Ser Arg Leu Val
                      -40                      -35                      -30

Lys Pro Ser Gln Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser
                      -25                      -20                      -15

Leu Val Ala Glu Leu Leu Leu Gly Ala Gly Ser Gly Ser His Leu Gly
                      -10                      -5                      1

Arg Ala Trp Ser Gly Leu Gly Ser Ser Ile Ile Glu Ala Ile Val Gly
5                      10                      15                      20

```

Val Leu Leu Thr Ile Arg Pro Ser Arg Leu Glu Pro Pro Tyr His Trp
 25 30 35
 Thr Ser Pro Ala
 40

(2) INFORMATION FOR SEQ ID NO: 471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo. Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq QFILLGTTSVVTA/AL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 471:

Met Glu Ser Gly Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly
 -20 -15 -10
 Thr Thr Ser Val Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys
 -5 1 5
 Ala Arg Val Ser Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly
 10 15 20 25
 Glu Asp Leu Lys Ser Ile Leu Ser Glu Xaa Pro Gly Lys Cys Val Pro
 30 35 40
 Tyr Ala Val Ile Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn
 45 50 55
 Ser Gln Phe Val Glu Asn Cys Lys
 60 65

(2) INFORMATION FOR SEQ ID NO: 472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq IYIICFXLPPLFS/FN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 472:

Met Gln Val Cys Arg Cys Ile Tyr Ile Ile Cys Phe Xaa Leu Pro Pro
 -15 -10 -5

Leu Phe Ser Phe Asn
 1

(2) INFORMATION FOR SEQ ID NO: 473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq QRLLLRFLASVIS/RK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473:

Met Ala Gln Arg Leu Leu Leu Arg Phe Leu Ala Ser Val Ile Ser Arg
 -15 -10 -5 1

Lys Pro Ser Gln Gly Gln Trp Ala Thr Pro His Phe Gln Ser Pro Ala
 5 10 15

Asp Pro Thr Met Gln Ser Trp Trp Pro Asp Cys Asn Thr Gln Pro Ser
 20 25 30

Pro Asp
 35

(2) INFORMATION FOR SEQ ID NO: 474:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 46 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Cancerous prostate
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -40..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.9
 seq FLWLITRPQPVLP/LL
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 474:

Met Leu Phe Ile Phe Asn Phe Leu Phe Ser Pro Leu Pro Thr Pro Ala
-40 -35 -30 -25

Leu Ile Cys Ile Leu Thr Phe Gly Ala Ala Ile Phe Leu Trp Leu Ile
 -20 -15 -10

Thr Arg Pro Gln Pro Val Leu Pro Leu Leu Asp Leu Asn Xaa
 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 475:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 49 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Hypertrophic prostate
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -46..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.9
 seq SHMLQLLP SKALC/LF
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475:

Met Tyr Pro Lys Trp Glu Ala Pro Val Thr Phe Cys Gln Leu Lys Arg
-45 -40 -35

Glu Lys Asp Pro Pro His Pro Ala His Ser Pro Phe Leu Gln Pro Arg
-30 -25 -20 -15

Phe Ser His Met Leu Gln Leu Leu Pro Ser Lys Ala Leu Cys Leu Phe
 -10 -5 1

Phe

(2) INFORMATION FOR SEQ ID NO: 476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -44..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7
seq LAERLGLFEELWA/AQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476:

Met Ala Leu Tyr Gln Arg Trp Arg Cys Leu Arg Leu Gln Gly Leu Gln
 -40 -35 -30

Ala Cys Arg Leu His Thr Ala Val Val Ser Thr Pro Pro Arg Trp Leu
 -25 -20 -15

Ala Glu Arg Leu Gly Leu Phe Glu Glu Leu Trp Ala Ala Gln Val Lys
 -10 -5 1

Arg Leu Ala Ser Met Ala Gln Lys Glu Pro Gln Thr
 5 10 15

(2) INFORMATION FOR SEQ ID NO: 477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 13.8
seq XGLLLFLLPGSLG/AE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477:

```

Met Gly Val Pro Arg Pro Gln Pro Trp Ala Xaa Gly Leu Leu Leu Phe
      -20                      -15                      -10

Leu Leu Pro Gly Ser Leu Gly Ala Glu Ser His Leu Ser Leu Leu Tyr
      -5                      1                      5

His Leu Thr Ala Val Ser Ser Pro Ala Pro Gly Thr Pro Ala Phe Trp
  10                      15                      20                      25

Val Ser Gly Trp Leu Gly Pro Gln Gln Tyr Pro Ser Xaa
      30                      35

```

(2) INFORMATION FOR SEQ ID NO: 478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -45..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 13.4
seq LVLALXLVSAALS/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478:

```

Met Ala Ala Ala Val Pro Lys Arg Met Arg Gly Pro Ala Gln Ala Lys
-45                      -40                      -35                      -30

Leu Leu Pro Gly Ser Ala Ile Gln Ala Leu Val Gly Leu Ala Arg Pro
      -25                      -20                      -15

Leu Val Leu Ala Leu Xaa Leu Val Ser Ala Ala Leu Ser Ser Val Val
      -10                      -5                      1

Ser Arg Thr Asp Ser Pro Ser Pro Thr Val Leu Asn Ser His Ile Ser
  5                      10                      15

Thr Pro Asn Val Asn Ala Leu Thr His Glu Asn Gln Thr Lys Pro Ser
  20                      25                      30                      35

Ile Ser Gln Ile Ser Thr Thr Leu Pro Pro Xaa Xaa Ser Thr Lys Xaa
      40                      45                      50

```

Ser Gly Gly Ala Xaa Val Val Pro His Pro Ser Pro Gly
55 60

(2) INFORMATION FOR SEQ ID NO: 479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 13
seq LLLVLLLVTXRS/MP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479:

Met Trp Leu Trp Glu Asp Gln Gly Gly Leu Leu Gly Pro Phe Ser Phe
-25 -20 -15
Leu Leu Leu Val Leu Leu Leu Val Thr Arg Xaa Arg Ser Met Pro Ala
-10 -5 1
Ser Ser Pro Ala Ala Ser Ser Phe Tyr Cys Ala Ser Ser Ala Xaa Ser
5 10 15
Arg Cys Pro Leu Ala Gly Pro Cys Arg Cys Ser Ser Pro Gly Thr Ala
20 25 30 35
Phe Leu

(2) INFORMATION FOR SEQ ID NO: 480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 11.6
seq LLLLVQLLRFLRA/DG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 480:

```

Met Asn Trp Glu Leu Leu Leu Trp Leu Leu Val Leu Cys Ala Leu Leu
    -25                      -20                      -15

Leu Leu Leu Val Gln Leu Leu Arg Phe Leu Arg Ala Asp Gly Asp Leu
    -10                      -5                      1

Thr Leu Leu Trp Ala Glu Trp Gln Gly Arg Arg Pro Glu Trp Glu Leu
    5                      10                      15                      20

Thr Asp Met Val Val Trp Val Thr Gly Ala Ser Ser Gly Ile Gly Glu
    25                      30                      35

Glu Leu Ala Tyr Gln Leu Ser Lys Leu Gly Val Ser Leu Val Leu Ser
    40                      45                      50

Ala Arg

```

(2) INFORMATION FOR SEQ ID NO: 481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.2
seq AFLLLVALSYTLA/RD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481:

```

Met Glu Lys Ile Pro Val Ser Ala Phe Leu Leu Leu Val Ala Leu Ser
-20                      -15                      -10                      -5

Tyr Thr Leu Ala Arg Asp Thr Thr Val Lys Pro Gly Ala Lys Lys Asp
    1                      5                      10

Thr Lys Asp Ser Arg Pro Lys Leu Pro Gln Thr Leu Ser Arg Gly Trp
    15                      20                      25

Gly Asp Gln Leu Ile Trp Thr Arg
    30                      35

```

(2) INFORMATION FOR SEQ ID NO: 482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -40..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.2
seq AFLLLVALSYTLA/RD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482:

```

Met Ser Asn Tyr Thr Asp Ala Glu Ser Ser Phe Ser Lys Gln Glu Ile
-40                -35                -30                -25

Ile Arg Val Ala Met Glu Lys Ile Pro Val Ser Ala Phe Leu Leu Leu
                -20                -15                -10

Val Ala Leu Ser Tyr Thr Leu Ala Arg Asp Thr Thr Val Lys Pro Gly
                -5                1                5

Ala Lys Lys Asp Thr Lys Asp Ser Arg Pro Lys Pro Pro Arg
 10                15                20

```

(2) INFORMATION FOR SEQ ID NO: 483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -53..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.6
seq FILLIFIAEVAA/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 483:

Met	Asn	Trp	Glu	Leu	Leu	Leu	Trp	Leu	Leu	Val	Leu	Cys	Ala	Leu	Leu
			-25					-20					-15		
Leu	Leu	Leu	Val	His	Leu	Leu	Arg	Phe	Leu	Arg	Ala	Asp	Gly	Asp	Leu
		-10					-5					1			
Thr	Leu	Leu	Trp	Ala	Glu	Trp	Gln	Gly	Arg	Arg	Pro	Glu	Trp	Glu	Leu
5					10					15					20
Thr	Asp	Met	Val	Val	Trp	Val	Thr	Gly	Ala	Ser	Ser	Gly	Ile	Gly	Glu
			25						30					35	
Glu	Leu	Ala	Tyr	Gln	Leu	Ser	Lys	Leu	Gly	Xaa	Ser	Leu	Val	Leu	Ser
			40					45					50		

Ala Arg Arg Val His Glu Leu Glu Arg Val Lys Arg Arg Cys Leu Glu
 55 60 65
 Asn Gly Asn Leu Xaa Glu Lys Asp Ile Leu Val Leu Pro Leu Gly
 70 75 80

(2) INFORMATION FOR SEQ ID NO: 485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -51..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.3
seq VSCLTLWSPGCWP/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 485:

Met Thr Thr Phe Leu Pro Val Pro Gln Met Met Ala Gly Phe Ser Phe
 -50 -45 -40
 Gly Thr Phe Gly Asn Pro Pro Met Glu Ser Pro Ser Ala Trp Gln Thr
 -35 -30 -25 -20
 Ile His Gln Pro Phe Ile Val Ser Cys Leu Thr Leu Trp Ser Pro Gly
 -15 -10 -5
 Cys Trp Pro Gln Pro Ile Gln Arg Lys Glu Trp Asp Ser Gly Thr Phe
 - 1 5 10
 Glu Asn Leu Arg Val Leu Ser Cys Ala Met Val Glu
 15 20 25

(2) INFORMATION FOR SEQ ID NO: 486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.5
seq LVXFSLLTAILG/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 486:

```

Met Ala Ser Lys Gly Met Arg His Phe Cys Leu Ile Ser Glu Gln Leu
      -25              -20              -15

Val Xaa Phe Ser Leu Leu Ala Thr Ala Ile Leu Gly Ala Val Ser Trp
      -10              -5              1

Gln Pro Thr Asn Gly Ile Phe Leu Ser Met Phe Leu Ile Val Leu Pro
      5              10              15              20

Leu Glu Ser Met Ala His Gly Leu Phe His Glu Leu Gly Asn Cys Leu
      25              30              35

Gly Gly Thr Ser Val Gly Tyr Ala Ile Val Ile Pro Thr Asn Phe Cys
      40              45              50

Ser Pro Asp Gly Gln Pro Thr Leu Leu Pro Pro Glu His Val Gln Glu
      55              60              65

Leu Asn Leu Arg Ser Thr Gly Met Leu Asn Ala Ile Gln Arg Phe Phe
      70              75              80

Ala Tyr His Met Ile Glu Thr Tyr Gly Cys Asp Tyr Ser Thr Ser Gly
      85              90              95              100

Leu

```

(2) INFORMATION FOR SEQ ID NO: 487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.3
seq VLPVILLLLGAHP/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 487:

Met Ala Ala Ala Ala Trp Leu Gln Val Leu Pro Val Ile Leu Leu Leu
 -20 -15 -10

Leu Gly Ala His Pro Ser Pro Leu Ser Phe Phe Ser Ala Gly Pro Ala
 -5 1 5 10

Thr Val Ala Ala Ala Asp Arg Ser Lys Trp His Xaa Pro Ile Pro Ser
 15 20 25

Gly Lys Asn Tyr Phe Ser Phe Gly Lys Ile Leu Phe Arg Asn Thr Thr
 30 35 40

Ile Phe Leu Lys Phe Asp Gly Glu Arg
 45 50

(2) INFORMATION FOR SEQ ID NO: 488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -109..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.1
seq LVLAVLFFHQLVG/DP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488:

Met Ala Ser Pro Arg Thr Val Thr Ile Val Ala Leu Ser Val Ala Leu
 - -105 -100 -95

Gly Leu Phe Phe Val Phe Met Gly Thr Ile Lys Leu Thr Pro Arg Leu
 -90 -85 -80

Ser Lys Asp Ala Tyr Ser Glu Met Lys Arg Ala Xaa Lys Ser Tyr Val
 -75 -70 -65

Arg Ala Leu Pro Leu Leu Lys Lys Met Gly Ile Asn Ser Ile Leu Leu
 -60 -55 -50

Arg Lys Ser Ile Gly Ala Leu Glu Val Ala Cys Gly Ile Val Met Thr
 -45 -40 -35 -30

Leu Val Pro Gly Arg Pro Lys Asp Val Ala Asn Phe Phe Leu Leu Leu
 -25 -20 -15

Leu Val Leu Ala Val Leu Phe Phe His Gln Leu Val Gly Asp Pro Leu
 -10 -5 1

Lys

(2) INFORMATION FOR SEQ ID NO: 489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -38..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.8
seq LLLLCALHSHIYC/IK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489:

Met Pro Asn Leu Ser Phe Gly Gly Leu Asp Thr Asn Gln Met Arg Val
 -35 -30 -25

Asn Phe Leu Ser Val Asp Val Cys Lys Leu Leu Leu Leu Cys Ala Leu
 -20 -15 -10

His Ser His Ile Tyr Cys Ile Lys Gln Ser Ala Leu Arg
 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -55..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.8
seq XXLLLLNVGQLLA/QT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490:

Met Gly Pro Pro Met Leu Gln Glu Ile Ser Asn Leu Phe Leu Ile Leu
 -55 -50 -45 -40

Leu Met Met Gly Ala Ile Phe Thr Leu Ala Ala Leu Lys Glu Ser Leu
 -35 -30 -25

Ser Thr Cys Ile Pro Ala Ile Val Cys Leu Xaa Xaa Leu Leu Leu Leu
 -20 -15 -10

Asn Val Gly Gln Leu Leu Ala Gln Thr Lys Lys Val Val Arg Pro Thr
 -5 1 5

Arg Lys Lys Thr Leu Ser Thr
 10 15

(2) INFORMATION FOR SEQ ID NO: 491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -71..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.6
seq VVXFLLLLAXLIA/TY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491:

Met Xaa Xaa Phe Thr Asp Pro Ser Ser Val Asn Glu Lys Lys Arg Arg
 -70 -65 -60

Glu Arg Glu Glu Arg Gln Asn Ile Val Leu Trp Arg Gln Pro Leu Ile
 -55 -50 -45 -40

Thr Leu Gln Tyr Phe Ser Leu Glu Ile Leu Val Ile Leu Lys Glu Trp
 -35 -30 -25

Thr Ser Lys Leu Trp His Arg Xaa Xaa Ile Val Val Xaa Phe Leu Leu
 -20 -15 -10

Leu Leu Ala Xaa Leu Ile Ala Thr Tyr Tyr
 -5 1

(2) INFORMATION FOR SEQ ID NO: 492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids

(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -15..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.6
seq LLRGLLWXQVLCA/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 492:

Met Pro Leu Leu Arg Gly Leu Leu Trp Xaa Gln Val Leu Cys Ala Gly
-15 -10 -5 1

Pro Leu His Thr Glu
5

(2) INFORMATION FOR SEQ ID NO: 493:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -20..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.4
seq AVVGCLLVPPAEA/NK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493:

Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro
-20 -15 -10 -5

Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Xaa Cys Lys Cys Ile
1 5 10

Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val
15 20 25

Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val
30 35 40

Pro
45

(2) INFORMATION FOR SEQ ID NO: 494:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -24..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 7.9
seq LLLPRVLLTMASG/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 494:

Met Pro Ala Leu Leu Pro Val Ala Ser Arg Leu Leu Leu Leu Pro Arg
 -20 -15 -10

Val Leu Leu Thr Met Ala Ser Gly Ser Pro Pro Thr Gln Pro Ser Pro
 -5 1 5

Ala Ser Asp Ser Gly Ser Gly Tyr Val Pro Gly Ser Val Ser Ala Ala
 10 15 20

Phe Val Thr Cys Pro Asn Glu Lys Val Ala Lys Glu Ile Ala Arg Ala
 25 30 35 40

Val Gly Glu Lys Arg
 45

(2) INFORMATION FOR SEQ ID NO: 495:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 119 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide

(B) LOCATION: -108..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.9
 seq LLGLLSAEQLAEA/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 495:

```

Met Cys Leu Leu Leu Gly Ala Thr Gly Val Gly Lys Thr Leu Leu Val
      -105                -100                -95

Lys Arg Leu Gln Glu Val Ser Ser Arg Asp Gly Lys Gly Asp Leu Gly
      -90                -85                -80

Glu Pro Pro Pro Thr Arg Pro Thr Val Gly Thr Asn Leu Thr Asp Ile
      -75                -70                -65

Val Ala Gln Arg Lys Ile Thr Ile Arg Glu Leu Gly Gly Cys Met Gly
      -60                -55                -50                -45

Pro Ile Trp Ser Ser Tyr Tyr Gly Asn Cys Arg Ser Leu Leu Phe Val
      -40                -35                -30

Met Asp Ala Ser Asp Pro Thr Gln Leu Ser Ala Xaa Xaa Val Gln Leu
      -25                -20                -15

Leu Gly Leu Leu Ser Ala Glu Gln Leu Ala Glu Ala Ser Val Leu Ile
      -10                -5                1

Leu Phe Asn Lys Ile Asp Asn
  5                10
  
```

(2) INFORMATION FOR SEQ ID NO: 496:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -41..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.7
 seq LLCLGQLHHPGLG/RV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496:

```

Met Glu Leu Pro Ala Val Asn Leu Glu Ser Asp Ser Pro Arg Ser Leu
      -40                -35                -30

Ala Ala Asp Asn Leu Gly Leu His Cys Ile Leu Arg Leu Leu Cys Leu
  
```

-25 -20 -15 -10

Gly Gln Leu His His Pro Gly Leu Gly Arg Val Gly Cys Gly Ser Ala

 -5 1 5

Gly Leu His Arg Arg Arg

 10

(2) INFORMATION FOR SEQ ID NO: 497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -51..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6
seq PALILLFALGSLG/SG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 497:

Met Ala Phe Leu Arg Lys Val Tyr Ser Ile Leu Ser Leu Gln Val Leu

-50 -45 -40

Leu Thr Thr Val Thr Ser Thr Val Phe Leu Tyr Phe Glu Ser Val Arg

-35 -30 -25 -20

Thr Phe Val His Glu Ser Pro Ala Leu Ile Leu Leu Phe Ala Leu Gly

 -15 -10 -5

Ser Leu Gly Ser Gly

 1

(2) INFORMATION FOR SEQ ID NO: 498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -29..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.6
 seq PTLAIALAANAWA/FV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498:

Met Tyr Thr Tyr Gly Asn Lys Gln His Asn Ser Pro Thr Trp Asp Asp
 -25 -20 -15

Pro Thr Leu Ala Ile Ala Leu Ala Ala Asn Ala Trp Ala Phe Val Leu
 -10 -5 1

Phe Tyr Val Ile Pro Glu Val Ser Gln Val Thr Lys Ser Ser Pro Glu
 5 10 15

Gln Ser Tyr Gln Gly Asp Met Tyr Pro Thr Arg Asp Leu
 20 25 30

(2) INFORMATION FOR SEQ ID NO: 499:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -32..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.6
 seq WILVLALPLTVWP/WL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499:

Met Gln Gln Ile Phe Ile Gln Gln Cys Arg Glu Leu Asn Phe Trp Ser
 -30 -25 -20

Arg Glu Pro Trp Ile Leu Val Leu Ala Leu Pro Leu Thr Val Trp Pro
 -15 -10 -5

Trp Leu Ser Pro Glu Ala Gln Pro Pro Leu
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 500:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids

- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -15...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.5
seq AVLLALLMAGLAL/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500:

```
Met Lys Ala Val Leu Leu Ala Leu Leu Met Ala Gly Leu Ala Leu Gln
-15                      -10                      -5                      1
Pro Gly Thr Ala Leu Leu Cys Tyr Ser Trp Xaa Ala Gln Val Xaa Asn
           5                      10                      15
Glu Asp Cys Leu Gln Val Glu Asn Cys Thr Gln Leu Gly Glu Gln Cys
           20                      25                      30
Trp Thr Ala Arg Ile Arg Ala Val Gly Leu Leu Thr Val Ile Ser Lys
           35                      40                      45
Gly Cys Ser Leu Asn Cys Val Asp Xaa Ser Gln Asp Tyr Tyr Val Gly
           50                      55                      60                      65
Lys Lys Asn Ile Thr Cys Cys Asp
                      70
```

(2) INFORMATION FOR SEQ ID NO: 501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.1
seq QACLLGLFALILS/GK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501:

Met Gly Leu Gln Ala Cys Leu Leu Gly Leu Phe Ala Leu Ile Leu Ser
 -15 -10 -5
 Gly Lys Cys Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr Leu Pro
 1 5 10 15
 Pro Gly Trp Val Ser Leu Gly Arg Ala Asp Pro Glu Glu Glu Leu Ser
 20 25 30
 Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg Leu Ser Glu Leu
 35 40 45
 Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln Tyr Gly Lys Tyr Leu
 50 55 60
 Thr Arg
 65

(2) INFORMATION FOR SEQ ID NO: 502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7
seq LGSGLGLSPGTSS/GR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502:

Met Arg Pro Gly Gln Val Ser Leu Leu Gly Pro Asp Ala Val Ser Val
 -25 -20 -15
 Leu Gly Ser Gly Leu Gly Leu Ser Pro Gly Thr Ser Ser Gly Arg Asn
 -10 -5 1
 Pro Asp Pro Gly Ser Gly Pro Gly Thr Leu Pro Xaa Xaa Ser Xaa Gln
 5 10 15
 Asn Pro Ser Pro Ala Pro Asp Pro Pro Pro Ala Leu Leu Leu Trp Asn
 20 25 30 35
 Leu Leu Thr Gln Arg Leu Gly Thr Thr Leu Val Pro Thr Leu Cys Pro
 40 45 50
 Ala Gln Thr Leu Ile Leu Cys Pro Ala Gln Thr Leu Ile Leu Cys Pro
 55 60 65

Xaa Leu Ile Pro Thr Leu Cys Pro Ala Leu Xaa Pro Val Leu Pro Xaa
 70 75 80
 Val Ala Leu Ser Ala Gln Pro Ser Leu Pro Ala Arg Val Gln Ser
 85 90 95

(2) INFORMATION FOR SEQ ID NO: 503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -33..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.8
seq FTSASLLLPMTG/MP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503:

Met Ile Asn Pro Ser Val Pro Ser Lys Ser Asn Ser His Pro Phe Leu
 -30 -25 -20
 Ser Thr Val Met Phe Thr Ser Ala Ser Leu Leu Leu Pro Met Ser Thr
 -15 -10 -5
 Gly Met Pro Thr Gln Asn Cys Phe Thr Pro Lys
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -68..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7

seq IACLAWWIGGGSG/XN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 504:

```

Met Ser Glu Lys Glu Xaa Asn Phe Pro Pro Leu Pro Lys Phe Ile Pro
      -65                      -60                      -55

Val Lys Pro Cys Phe Tyr Gln Asn Phe Ser Asp Glu Ile Pro Val Glu
      -50                      -45                      -40

His Gln Val Leu Val Lys Arg Ile Tyr Arg Leu Trp Met Phe Tyr Cys
      -35                      -30                      -25

Ala Thr Leu Gly Val Asn Leu Ile Ala Cys Leu Ala Trp Trp Ile Gly
      -20                      -15                      -10                      -5

Gly Gly Ser Gly Xaa Asn Phe Gly Leu Ala Phe Val Trp Leu Leu Leu
      1                      5                      10

Phe Thr Pro Cys Gly Tyr Val Cys Trp Phe Arg Pro Val Tyr Lys Ala
      15                      20                      25

Phe Arg Ala Asp Ser Ser Phe Asn Phe Met Ala Leu
      30                      35                      40

```

(2) INFORMATION FOR SEQ ID NO: 505:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7
seq ILRLYFFLQLAHS/GY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 505:

```

Met Asn Pro Thr Lys Leu Ile Leu Lys Thr Ile Leu Arg Leu Tyr Phe
      -20                      -15                      -10

Phe Leu Gln Leu Ala His Ser Gly Tyr Thr Lys Leu Gln Lys Lys Tyr
      -5                      1                      5

Met Lys Ser Arg Tyr Glu Gln Val Asp Leu Val Gly Lys Met Xaa Gln
      10                      15                      20                      25

Lys Ala Ala Thr Thr Val Xaa His Leu Ala Ile Gln Cys His Trp

```

30

35

40

(2) INFORMATION FOR SEQ ID NO: 506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7
seq SXXCFVSVPPASA/IP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 506:

Met Ala Ser Ser Ser Pro Asp Ser Pro Cys Ser Xaa Xaa Cys Phe Val
 -20 -15 -10

Ser Val Pro Pro Ala Ser Ala Ile Pro Xaa Val Xaa Xaa Ala Xaa Asn
 -5 1 5

Ser Asp Xaa Pro Arg Asp Glu Val Gln Glu Val Val Phe Val Pro Ala
10 15 20 25

Gly Thr His Thr Pro Gly Ser Arg Leu Gln Cys Thr Tyr Ile Glu Val
 30 35 40

Glu Gln Val Ser Lys Thr His Ala Val Ile Leu Ser Arg Pro Ser Trp
 45 50 55

Leu Trp Gly Ala Glu Met Gly Xaa Thr Ser Met Val Ser Ala Leu Ala
 60 65 70

Thr Arg Leu Cys Gly Arg Arg Ser Gln Leu Gly Arg Ala Xaa Ala Leu
75 80 85

Leu Gly Met Asp Leu Leu Arg Cys Arg Pro Cys
90 95 100

(2) INFORMATION FOR SEQ ID NO: 507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -39..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.7
seq XLIAXLEPPGAMA/VR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 507:

```

Met Xaa Pro Val Leu Ala Ala Leu Ala His Val Leu Cys Pro Tyr Met
      -35                      -30                      -25

Ala Pro Gly Leu Cys Arg Glu Pro Ile Arg Xaa Leu Ile Ala Xaa Leu
      -20                      -15                      -10

Glu Pro Pro Gly Ala Met Ala Val Arg Arg Leu Pro Ser Ala
      -5                      1                      5

```

(2) INFORMATION FOR SEQ ID NO: 508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -45..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.7
seq PMLGLAAFRWIWS/RE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 508:

```

Met Asn Asn Leu Asn Asp Pro Pro Asn Trp Asn Ile Arg Pro Asn Ser
-45                      -40                      -35                      -30

Arg Ala Asp Gly Gly Asp Gly Ser Arg Trp Asn Tyr Ala Leu Leu Val
      -25                      -20                      -15

Pro Met Leu Gly Leu Ala Ala Phe Arg Trp Ile Trp Ser Arg Glu Ser
      -10                      -5                      1

Gln Lys Glu Val Glu Lys Glu Arg Glu Ala Tyr Arg Arg Arg Thr Ala
      5                      10                      15

```

Ala Phe Gln Gln Asp Leu Glu Ala Lys Tyr His Ala Met Ile Ser Xaa
20 25 30 35
Asn Arg Arg Ala Val
40

(2) INFORMATION FOR SEQ ID NO: 509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.6
seq AALCSLFFFLSLQ/EI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 509:

Met Leu Leu Leu Phe Leu Ala Ala Leu Cys Ser Leu Phe Phe Phe Leu
-15 -10 -5
Ser Leu Gln Glu Ile Ala Pro Gln Asp Pro Lys Pro Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -47..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.5
seq IIVCLFAFLVAHC/FL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 510:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq LFCVLLSLRPHTS/GT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 512:

```

Met Gln Asn Phe Cys His His Leu Ala Ile Cys Thr Val Ile Leu Phe
   -25                      -20                      -15

Cys Val Leu Leu Ser Leu Arg Pro His Thr Ser Gly Thr Leu Trp Ala
   -10                      -5                      1                      5

Ser Ser Ala His Gly Leu His Leu Ala Pro Ala Glu Pro Gln Leu Ser
          10                      15                      20

Cys Trp Met Cys Cys Ala
          25

```

(2) INFORMATION FOR SEQ ID NO: 513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -64..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq VLMRLVASAYSIA/QK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 513:

```

Met Pro Ser Phe Ser Lys Asp Leu Leu Thr Val Pro Lys Leu Gly Thr
          -60                      -55                      -50

Gly His Xaa Xaa Gly Xaa Gly Ser Tyr Asp Xaa Ala Leu Xaa Leu Leu
          -45                      -40                      -35

Leu Lys Cys Leu Trp Ser Asn Val Val Pro Glu Cys Thr Met Ala Ser
          -30                      -25                      -20

Ser Asn Thr Val Leu Met Arg Leu Val Ala Ser Ala Tyr Ser Ile Ala
          -15                      -10                      -5

Gln Lys Ala Gly Met Ile Val Arg Arg Val Ile Ala Glu Gly Asp Leu

```

1 5 10 15
Gly Ile Val Glu Lys Thr Cys Ala Thr Asp Leu Gln Thr Lys Ala Asp
 20 25 30
Arg Leu Ala Gln Met Ser Ile Cys Ser Ser Leu Xaa Xaa Lys Phe Pro
 35 40 45
Lys Leu Xaa Ile Ile Gly Glu Glu Asp Leu Pro Ser Glu Glu Val Asp
 50 55 60
Gln Glu Leu Ile Glu Asp Xaa
65 70

(2) INFORMATION FOR SEQ ID NO: 514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.2
seq LEMXLAFASHIXA/RD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 514:

Met Arg Gly Ala His Leu Thr Ala Leu Glu Met Leu Xaa Ala Phe Ala
-20 -15 -10
Ser His Ile Xaa Ala Arg Asp Ala Ala Gly Ser Gly
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -139..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.2
seq FGLLHQLSQCVTS/LE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 515:

Met Glu Val Gly Leu Pro Ala Ile Thr Leu Phe Leu Thr Ser Ala Ser
-135 -130 -125
Ser Pro Val Val Ala Thr Thr Met Asp Gln Glu Pro Val Gly Gly Val
-120 -115 -110
Glu Arg Gly Glu Ala Val Ala Ala Ser Gly Xaa Ala Ala Ala Ala Ala
-105 -100 -95
Phe Gly Glu Ser Ala Gly Gln Met Ser Asn Glu Arg Gly Phe Glu Asn
-90 -85 -80
Val Glu Leu Gly Val Ile Gly Lys Lys Lys Lys Val Pro Arg Arg Val
-75 -70 -65 -60
Ile His Phe Val Ser Gly Glu Thr Met Glu Glu Tyr Ser Thr Asp Glu
-55 -50 -45
Asp Xaa Val Asp Gly Leu Glu Lys Xaa Met Phe Cys Leu Leu Leu Ile
-40 -35 -30
Arg Gln Asn Leu Pro Gly Val Pro Thr Tyr Gly Phe Thr Cys Phe Gly
-25 -20 -15
Leu Leu His Gln Leu Ser Gln Cys Val Thr Ser Leu Glu
-10 -5 1

(2) INFORMATION FOR SEQ ID NO: 516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -43..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.1
seq SAATLASLGGTSS/RR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 516:

Met Lys Glu Leu Glu Arg Gln Gln Lys Glu Val Glu Glu Arg Pro Glu
 -40 -35 -30

Lys Asp Phe Thr Glu Lys Gly Ser Arg Asn Met Pro Gly Leu Ser Ala
 -25 -20 -15

Ala Thr Leu Ala Ser Leu Gly Gly Thr Ser Ser Arg Arg Gly Ser Gly
 -10 -5 1 5

Asp Thr Ser Ile Ser Ile Asp Pro Glu
 10

(2) INFORMATION FOR SEQ ID NO: 517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.1
seq VLVILCIIVTVCVT/IV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 517:

Met Ser Met Gly Phe Met Met Leu Val Leu Val Ile Leu Cys Ile Val
 -20 -15 -10

Thr Val Cys Val Thr Ile Val Cys Thr Tyr Phe Leu Leu Asn Ala Glu
 -5 - 1 5 10

Asp Tyr Arg Trp Gln Trp Thr Ser Phe Leu Ser Ala Ala Ser Thr Ala
 15 20 25

Ile Tyr Val Tyr Met Tyr Ser Phe Tyr Tyr Tyr Phe Phe Lys Thr Lys
 30 35 40

Met Tyr Gly Leu Phe Gln Thr Ser Phe Tyr Phe Gly Tyr Met Ala Val
 45 50 55

Phe Ser Thr Ala Leu Gly Ile Met Cys Gly Ala Ile
 60 65 70

(2) INFORMATION FOR SEQ ID NO: 518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids

(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -70..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6
seq LLFPLTLVRSFWS/DM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 518:

Met Met Glu Leu Xaa Leu Lys Xaa Xaa Thr Lys Xaa Glu Xaa Glu Ser
-70 -65 -60 -55
Ala Cys Thr Glu Ala Tyr Ser Gln Ser Asp Glu Gln Tyr Ala Cys His
-50 -45 -40
Leu Gly Cys Gln Asn Gln Leu Pro Phe Ala Glu Leu Arg Gln Glu Gln
-35 -30 -25
Leu Met Ser Leu Met Pro Lys Met His Leu Leu Phe Pro Leu Thr Leu
-20 -15 -10
Val Arg Ser Phe Trp Ser Asp Met Met Asp Ser Ala Gln Ser Phe Xaa
-5 1 5 10
Thr Ser Ser Trp Thr Phe Tyr Leu Gln Ala Asp Xaa Gly Xaa Ile Val
15 20 25
Ile Xaa Gln Ser Lys Pro Glu Ile Gln Tyr Ala Pro His Leu Glu Gln
30 35 40
Glu

(2) INFORMATION FOR SEQ ID NO: 519:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -24..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 6
seq GLILLFASHLINQ/FS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 519:

Met Val Ser Asn Ala Ser Glu Thr Ser Cys Leu Gly Leu Ile Leu Leu
-20 -15 -10
Phe Ala Ser His Leu Ile Asn Gln Phe Ser Ser
-5 1

(2) INFORMATION FOR SEQ ID NO: 520:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -73..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6
seq LIVEFISVCTALLA/EG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 520:

Met Pro Arg Lys Arg Lys Cys Asp Leu Arg Ala Val Arg Val Gly Leu
-70 -65 -60
Leu Leu Gly Gly Gly Gly Val Tyr Gly Ser Arg Phe Arg Phe Thr Phe
-55 -50 -45
Pro Gly Cys Arg Ala Leu Ser Pro Trp Arg Val Arg Xaa Gln Arg Arg
-40 -35 -30
Arg Cys Glu Met Ser Thr Met Phe Ala Asp Thr Leu Leu Ile Val Phe
-25 -20 -15 -10
Ile Ser Val Cys Thr Ala Leu Leu Ala Glu Gly Ile Thr Trp Val Leu
-5 1 5
Val Tyr Arg Thr Asp Lys Tyr Lys Arg Leu Lys Ala Glu Val Glu Lys
10 15 20
Gln Ser Lys Lys Tyr Leu Met Val Glu Trp Trp Gln Xaa Phe Leu Phe
25 30 35
Tyr Pro Ser Phe Leu Xaa Pro Lys Xaa Val Ser Ser
40 45 50

(2) INFORMATION FOR SEQ ID NO: 521:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq LGAAALALLLANT/DV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 521:

Met Gly Met Trp Ser Ile Gly Ala Gly Ala Leu Gly Ala Ala Ala Leu
 -20 -15 -10

Ala Leu Leu Leu Ala Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys
 -5 1 5

Ala Ala Leu Glu Tyr Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys
 10 15 20 25

Glu Pro Arg Thr Phe Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala
 30 35 40

Val Ile Met Ala Val Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu Glu
 45 50 55

Ala Ala Asp Leu Ser Ser Leu Lys Ser Met Leu Asp Gln Leu Gly Val
 - 60 65 70

Pro Leu Tyr Ala Val Val Lys Glu Gln Arg
 75 80

(2) INFORMATION FOR SEQ ID NO: 522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq LPLLLVANAGTAA/VG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 522:

Met Asp Val Ala Phe Leu Glu Xaa Leu Ile Lys Asp Asp Ile Glu Arg
-30 -25 -20

Gly Arg Leu Pro Leu Leu Leu Val Ala Asn Ala Gly Thr Ala Ala Val
-15 -10 -5 1

Gly His Thr Asp Lys Ile Gly Arg Leu Lys Glu Leu Cys Glu Gln Tyr
5 10 15

Gly Ile Trp Leu His Val Glu Gly Val Asn
20 25

(2) INFORMATION FOR SEQ ID NO: 523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.8
seq LFNLLWLALACSP/VW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 523:

Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro
-15 -10 -5

Val Trp
1

(2) INFORMATION FOR SEQ ID NO: 524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -33..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.8
seq FICLOWALPHSEA/GD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 524:

```

Met Asn Ala Gln Pro Gly Leu Xaa Leu Asp Cys Ile Thr Arg Phe Leu
      -30                      -25                      -20

Thr Xaa Gly Gln Phe Ile Cys Leu Gln Trp Ala Leu Pro His Ser Glu
      -15                      -10                      -5

Ala Gly Asp Phe Glu Ala Lys
  1                      5

```

(2) INFORMATION FOR SEQ ID NO: 525:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -69..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.7
seq LCRLCLVRLFCC/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 525:

```

Met Gly Lys Glu Trp Gly Trp Gln Glu Met Glu Asn Gly Gly Ala Ala
      -65                      -60                      -55

Pro Ala Trp Gly Ala Gly Pro Pro Val His Pro Ala Pro Pro Pro Val
      -50                      -45                      -40

Glu Lys Thr Leu Ser Trp Gly Cys Gly Phe Gly Leu His Ser Gly Phe
      -35                      -30                      -25

Gly Gly Ser Gly Gly Gly Val Gly Leu Cys Arg Leu Leu Cys Leu Val

```

-20

-15

-10

Arg Leu Phe Cys Cys Ser Ser Ile Leu Tyr Gln Arg Gln Lys
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7
seq AALLLTATVRLSA/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 526:

Met Ala Ala Pro Ser Gly Gly Trp Asn Gly Val Gly Ala Ser Leu Trp
-25 -20 -15

Ala Ala Leu Leu Leu Thr Ala Thr Val Arg Leu Ser Ala Ser Pro Gly
-10 -5 1

Pro

(2) INFORMATION FOR SEQ ID NO: 527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -48..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7
seq LLLFFGKLLVVGG/VG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 527:

[illegible]

(2) INFORMATION FOR SEQ ID NO: 528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -91..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.7
seq SVLELIVASVCQS/HI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 528:

Met Glu Arg Asn Cys Lys Gly Ser Phe Gly Val Ile Lys Glu Gly Asp
-90 -85 -80

Thr Asp Thr Xaa Glu Thr Lys Ala Arg Arg Thr Val Trp Glu Pro Arg
-75 -70 -65 -60

Gly Arg Tyr Ser Phe Arg Xaa Thr Pro Arg Pro Ala Tyr Pro Val Glu
-55 -50 -45

Gln Cys Gly Phe Ala Arg Arg Ala Leu Glu Leu Leu Glu Ile Arg Lys
 -40 -35 -30

His Ser Pro Glu Val Cys Glu Pro Pro Asn Ile Pro Val Thr Ser Val
 -25 -20 -15

Leu Glu Leu Ile Val Ala Ser Val Cys Gln Ser His Ile Arg Thr Thr
 -10 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -66..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7
seq LYMLAEALPVSHG/AH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 529:

Met Phe Val Glu Tyr Arg Lys Gln Leu Lys Leu Leu Leu Asp Arg Leu
 -65 -60 -55

Ala Gln Val Ser Pro Glu Leu Leu Leu Ala Ser Val Arg Arg Val Phe
 -50 -45 -40 -35

Ser Ser Thr Leu Gln Asn Trp Gln Thr Thr Arg Phe Met Glu Val Glu
 -30 -25 -20

Val Ala Ile Arg Leu Leu Tyr Met Leu Ala Glu Ala Leu Pro Val Ser
 -15 -10 -5

His Gly Ala His Phe Ser Gly Asp Val Ser Lys Ala Ser Ala Leu Gln
 1 5 10

Asp Met Met Arg Thr Leu Val Thr Ser Gly Val Ser Gly
 15 20 25

(2) INFORMATION FOR SEQ ID NO: 530:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -21..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.7
seq IIFLIQWHGSVFQ/EF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 530:

Met Leu Leu Gly Thr Ser Asn Ile Ile Ile Phe Leu Ile Gln Trp His
-20 -15 -10

Gly Ser Val Phe Gln Glu Phe
-5 1

(2) INFORMATION FOR SEQ ID NO: 531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -20..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.6
seq AFVXACVLSLIST/IY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 531:

Met Xaa Asn Arg Phe Ala Thr Ala Phe Val Xaa Ala Cys Val Leu Ser
-20 -15 -10 -5

Leu Ile Ser Thr Ile Tyr Met Ala Ala Ser Ile Gly Thr Asp Phe Trp
1 5 10

Tyr Glu Tyr Arg Ser Pro Val Gln Glu Asn Ser Ser Asp Leu Asn Lys
15 20 25

Ser Ile Trp Asp Glu Leu
30

(2) INFORMATION FOR SEQ ID NO: 532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -13..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq MSLTSGFLRVSQG/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 532:

Met Ser Leu Thr Ser Gly Phe Leu Arg Val Ser Gln Gly Ser Pro Asn
-10 -5 1
Leu Ser Gln
5

(2) INFORMATION FOR SEQ ID NO: 533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -63..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq AIRTLFSVTGILA/EQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 533:

Met Ala Asn Phe Lys Gly His Ala Leu Pro Gly Ser Phe Phe Leu Ile
-60 -55 -50
Ile Gly Leu Cys Trp Ser Val Lys Tyr Pro Leu Lys Tyr Phe Ser His
-45 -40 -35

Thr Arg Lys Asn Ser Pro Leu His Tyr Tyr Gln Arg Leu Glu Ile Val
 -30 -25 -20

Glu Ala Ala Ile Arg Thr Leu Phe Ser Val Thr Gly Ile Leu Ala Glu
 -15 -10 -5 1

Gln Phe Val Pro Asp Gly Pro His Leu His Leu Tyr His Glu Asn His
 5 10 15

Trp Ile Lys Leu Met Asn
 20

(2) INFORMATION FOR SEQ ID NO: 534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -52..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq AGLLFGSLAGLGA/YQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 534:

Met Gln Asp Thr Gly Ser Val Val Pro Leu His Trp Phe Gly Phe Gly
 -50 -45 -40

Tyr Ala Ala Leu Val Ala Ser Gly Gly Ile Ile Gly Tyr Val Lys Ala
 -35 -30 -25

Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser Leu Ala
 -20 -15 -10 -5

Gly Leu Gly Ala Tyr Gln Leu Ser Gln Asp Pro Arg Asn Val Trp Val
 1 5 10

Phe Leu Ala Thr Ser Gly Thr Leu Ala
 15 20

(2) INFORMATION FOR SEQ ID NO: 535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -35..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.4
seq CCALLTSLXCIWG/PA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 535:

```

Met Glu Xaa Gly Leu Lys Ser Ala Asp Pro Arg Asp Gly Thr Gly Tyr
-35                -30                -25                -20

Thr Xaa Xaa Xaa Xaa Tyr Cys Cys Ala Leu Leu Thr Ser Leu Xaa Cys
          -15                -10                -5

Ile Trp Gly Pro Ala Tyr Leu Gln Leu Ala His Gly Tyr Val Lys
          1                5                10

```

(2) INFORMATION FOR SEQ ID NO: 536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -42..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.4
seq ITGVILLAVGIWG/KV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 536:

```

Met Ala Ser Pro Ser Arg Arg Leu Gln Thr Lys Pro Val Ile Thr Cys
-40                -35                -30

Phe Lys Ser Val Leu Leu Ile Tyr Thr Phe Ile Phe Trp Ile Thr Gly
-25                -20                -15

Val Ile Leu Leu Ala Val Gly Ile Trp Gly Lys Val Ser Leu Glu Asn
-10                -5                1                5

Tyr Phe Ser Leu Leu Asn Glu Lys Ala Thr Asn Val Pro Phe Val Leu
          10                15                20

```

Ile Ala Thr Gly Thr Val Ile Ile Leu Leu Gly Thr Leu
 25 30 35

(2) INFORMATION FOR SEQ ID NO: 537:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -67..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.2
 seq LSVSLPCAGAWS/LL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 537:

Met Phe Ser Arg Glu Leu Ala Pro Thr Arg Ile Gly Gly Ala Ser Ser
 -65 -60 -55

Gly Ser Arg Ser Gly Gly Thr Leu Ile Ser Thr Ala Pro Leu Thr Thr
 -50 -45 -40

Arg Val Leu Asn Pro Thr Ala Gln Cys Phe Cys Leu Asp Cys Thr Leu
 -35 -30 -25 -20

Arg Arg Met Gln Thr His Leu Ser Val Ser Leu Leu Pro Cys Ala Gly
 -15 -10 -5

Ala Trp Ser Leu Leu Xaa Ser Lys Lys Val Ile Leu Pro Ser Cys Ser
 1 5 10

Ser Ile Leu Xaa Thr Val Val Val Ile
 15 20

(2) INFORMATION FOR SEQ ID NO: 538:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1
seq LLMLGVTLPNSYW/RV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 538:

```

Met Ser Met Ala Val Glu Thr Phe Gly Phe Phe Met Ala Thr Val Gly
      -25                      -20                      -15

Leu Leu Met Leu Gly Val Thr Leu Pro Asn Ser Tyr Trp Arg Val Ser
      -10                      -5                      1

Thr Val His Gly Asn Val Ile Xaa Thr Asn Xaa Ile Phe Glu Asn Leu
      5                      10                      15

Trp Phe Ser Ser Ala Gly
      20                      25

```

(2) INFORMATION FOR SEQ ID NO: 539:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq XFLXLXXLSXXWP/XD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 539:

```

Met Glu Lys Ile Pro Val Ser Xaa Phe Leu Xaa Leu Xaa Xaa Leu Ser
-20                      -15                      -10                      -5

Xaa Xaa Trp Pro Xaa Asp Thr Thr Val Lys Pro Gly Ala Xaa Lys Asp
      1                      5                      10

Thr Lys Asp Ser Arg Xaa Lys Leu Pro Gln Thr Leu Ser Arg Gly Trp
      15                      20                      25

Gly Asp Gln Leu Ile Trp Thr Arg
      30                      35

```

(2) INFORMATION FOR SEQ ID NO: 540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -67..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq LILERPLVPSAEA/SG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 540:

```

Met His Ser Ala Glu Glu Pro Leu Xaa Leu Ala Ala Leu Arg Gly Ala
  -65                      -60                      -55

Arg Gly His Leu Pro Cys Gly Ser Arg His His Val Gly Ser Leu Ala
  -50                      -45                      -40

Pro Ala Ser Val Pro Ala Pro Gly Ala Cys Leu Trp Val Cys Glu Trp
  -35                      -30                      -25                      -20

Glu Thr Leu Leu Pro Gly Leu Ile Leu Glu Arg Pro Leu Val Pro Ser
      -15                      -10                      -5

Ala Glu Ala Ser Gly Ala Gly Lys Leu Ser Arg Lys Glu Ala Leu Leu
      1                      5                      10

Ser Asn Tyr Ala Leu
  15

```

(2) INFORMATION FOR SEQ ID NO: 541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -43..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.9
seq GLWLALVDGLVRX/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 541:

```

Met Ala Gly Gln Phe Arg Ser Tyr Val Trp Asp Pro Leu Leu Ile Leu
      -40              -35              -30

Ser Gln Ile Val Leu Met Gln Thr Val Tyr Tyr Gly Ser Leu Gly Leu
      -25              -20              -15

Trp Leu Ala Leu Val Asp Gly Leu Val Arg Xaa Ala Pro Arg Trp Ile
      -10              -5              1              5

Xaa Gly

```

(2) INFORMATION FOR SEQ ID NO: 542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -78...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq V GAVFGLTTCISA/HV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 542:

```

Met Ala Pro Lys Val Phe Arg Gln Tyr Trp Asp Ile Pro Asp Gly Thr
      -75              -70              -65

Asp Cys His Arg Lys Ala Tyr Ser Thr Thr Ser Ile Ala Ser Val Ala
      -60              -55              -50

Gly Leu Thr Ala Ala Ala Tyr Arg Val Thr Leu Asn Pro Pro Gly Thr
      -45              -40              -35

Phe Leu Glu Gly Val Ala Lys Val Gly Gln Tyr Thr Phe Thr Ala Ala
      -30              -25              -20              -15

Ala Val Gly Ala Val Phe Gly Leu Thr Thr Cys Ile Ser Ala His Val
      -10              -5              1

Arg Glu Lys Pro Asp Asp Pro Leu Asn Arg
      5              10

```

(2) INFORMATION FOR SEQ ID NO: 543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq WLQVLPVILLLLG/VP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 543:

Met Ala Ala Ala Ala Trp Leu Gln Val Leu Pro Val Ile Leu Leu Leu
 -15 -10 -5

Leu Gly Val Pro Pro Ser
 1

(2) INFORMATION FOR SEQ ID NO: 544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -37..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq LLILD MNVLYTDA/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 544:

Met Glu Ile Tyr Phe Ile Phe Cys Ile Ile Val Pro Ile Ala Ala Ala
 -35 -30 -25

Thr Val Tyr Lys Ser Trp Cys Leu Leu Leu Ile Leu Asp Met Asn Val
 -20 -15 -10

Leu Tyr Thr Asp Ala Ser Pro Leu Gly
 -5 1

(2) INFORMATION FOR SEQ ID NO: 545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq VLLAIGMFFTAWF/FV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 545:

Met Ser Arg Tyr Thr Ser Pro Val Asn Pro Ala Val Phe Pro His Leu
 -30 -25 -20

Thr Val Val Leu Leu Ala Ile Gly Met Phe Phe Thr Ala Trp Phe Phe
 -15 -10 -5 1

Val Tyr Glu Val Thr Ser Thr Lys Tyr Thr Arg Asp Ile Tyr Lys Glu
 5 10 15

Leu Gln

(2) INFORMATION FOR SEQ ID NO: 546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -35..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq LMLSSSLPLLIWL/KD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 546:

```

Met Arg Leu Ala Ala Glu Ala His Pro Gly Arg Thr His Thr Leu Phe
-35                -30                -25                -20

Arg Arg Leu Lys Pro Phe Leu Met Leu Ser Ser Ser Leu Pro Leu Leu
                -15                -10                -5

Ile Trp Leu Lys Asp Arg
                1

```

(2) INFORMATION FOR SEQ ID NO: 547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -39..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq IILFSAIVGFIYG/YV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 547:

```

Met Leu Glu His Leu Xaa Ser Leu Pro Thr Gln Met Asp Tyr Lys Gly
                -35                -30                -25

Gln Lys Leu Ala Xaa Gln Met Phe Gln Gly Ile Ile Leu Phe Ser Ala
                -20                -15                -10

Ile Val Gly Phe Ile Tyr Gly Tyr Val Ala Glu Gln Phe Gly Trp Thr
                -5                1                5

Val Tyr Ile Val Met Ala Gly
10                15

```

(2) INFORMATION FOR SEQ ID NO: 548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -16..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.8
seq SKVLFCFSFSNVLG/FD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 548:

Met Glu Tyr Ser Lys Val Leu Phe Cys Ser Phe Ser Asn Val Leu Gly
-15 -10 -5

Phe Asp Tyr
1

(2) INFORMATION FOR SEQ ID NO: 549:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -26..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.7
seq LIMQLGSVLLTRC/PF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 549:

Met Ala Ser Lys Ile Gly Ser Arg Arg Trp Met Leu Gln Leu Ile Met
-25 -20 -15

Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp Gly Cys Phe
-10 -5 1 5

Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg Arg Lys Pro
10 15 20

Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Ser Gly
25 30

(2) INFORMATION FOR SEQ ID NO: 550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -52..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7
seq LGLALGRLEGGSA/RH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 550:

```
Met Glu His Tyr Arg Lys Ala Gly Ser Val Glu Leu Pro Ala Pro Ser
   -50                      -45                      -40

Pro Met Pro Gln Leu Pro Pro Asp Thr Leu Glu Met Arg Val Arg Asp
   -35                      -30                      -25

Gly Ser Lys Ile Arg Asn Leu Leu Gly Leu Ala Leu Gly Arg Leu Glu
   -20                      -15                      -10                      -5

Gly Gly Ser Ala Arg His Val Val Phe Ser Gly Ser Gly Arg Ala Ala
           1                      5                      10

Gly Lys Ala Val Ser Cys Ala Glu Ile Val Lys Arg Arg Val Pro
   15                      20                      25
```

(2) INFORMATION FOR SEQ ID NO: 551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq LIALTCLDGTTVS/AE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 551:

```
Met Asn Ala Leu Met Val Leu Phe Asn Val Thr Val Val Leu Ile Ala
```

-25 -20 -15
 Leu Thr Cys Leu Asp Gly Thr Thr Val Ser Ala Glu Met Ala Thr Met
 -10 -5 1 5
 Thr Met Gly Cys Phe His Gln Val Glu Asn Arg Val Lys Ile Leu Met
 10 15 20
 Ser Val Gly Pro Gly Gly Thr Ala Val Pro Met Ile Pro Phe Ala Ser
 25 30 35
 Ile Trp Met Ala Asp Met Ile Xaa Asp
 40 45

(2) INFORMATION FOR SEQ ID NO: 552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -45..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq VLVYLVTAERVWS/DD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 552:

Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val Asn Lys Tyr
 -45 -40 -35 -30
 Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe Ile Phe Arg
 -25 -20 -15
 Val Leu Val Tyr Leu Val Thr Ala Glu Arg Val Trp Ser Asp Asp His
 -10 -5 1
 Lys

(2) INFORMATION FOR SEQ ID NO: 553:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -16..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.5
seq SLFIYIFXTCSNT/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 553:

Met Ile Ile Ser Leu Phe Ile Tyr Ile Phe Xaa Thr Cys Ser Asn Thr
-15 -10 -5
Ser Pro Ser Tyr Gln Xaa Thr Gln Leu Gly Leu Gly Leu Pro Ser Ala
1 5 10 15
Gln Trp Trp Pro Leu Thr Gly Arg Arg Met Gln Cys Cys Arg Leu Phe
20 25 30
Cys Phe Xaa Leu Gln
35

(2) INFORMATION FOR SEQ ID NO: 554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -16..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.4
seq LNSLSALAEAVG/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 554:

Met Phe Arg Leu Asn Ser Leu Ser Ala Leu Ala Glu Leu Ala Val Gly
-15 -10 -5
Ser Arg Trp Tyr His Gly Gly Ser Gln Pro Ile Gln Ile Arg Arg Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 555:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 44 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Cancerous prostate
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -17..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.4
 seq TLRTWLCCAGSWA/VE
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 555:

Met Thr Ala Gly Thr Leu Arg Thr Trp Leu Cys Cys Ala Gly Ser Trp
 -15 -10 -5

Ala Val Glu Leu Pro Ala Glu Pro Leu Val Val Phe Cys Xaa Ser Thr
 1 5 10 15

Ser Arg Lys Arg Ala Lys Gly Leu Ile Gln Ser Val
 20 25

(2) INFORMATION FOR SEQ ID NO: 556:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Hypertrophic prostate
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -24..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.3
 seq RLLVILCVSVKAG/ST
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 556:

Met Leu Gly Arg Pro Cys Phe His Ser Pro Gln Arg Leu Leu Val Ile
 -20 -15 -10

Leu Cys Val Ser Val Lys Ala Gly Ser Thr
 -5 1

(2) INFORMATION FOR SEQ ID NO: 557:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq LQFVLPVATQIQQ/EV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 557:

Met Asp Glu Ala Arg Asp Asn Ala Cys Asn Asp Met Gly Lys Met Leu
-25 -20 -15
Gln Phe Val Leu Pro Val Ala Thr Gln Ile Gln Gln Glu Val Ile Lys
-10 -5 1

(2) INFORMATION FOR SEQ ID NO: 558:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq LCALGSAPSSMWA/GE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 558:

Met Ser Pro Ile Ser Ile Arg Glu Leu Cys Ala Leu Gly Ser Ala Pro
-20 -15 -10
Ser Ser Met Trp Ala Gly Glu
-5 1

(2) INFORMATION FOR SEQ ID NO: 559:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -13..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq MTDLLSASPWALT/IV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 559:

Met Thr Asp Leu Leu Ser Ala Ser Pro Trp Ala Leu Thr Ile Val Ser
-10 -5 1
Ser Glu Leu His Leu Ala Pro Ser Met Thr Thr Val Asp Gln Leu Glu
5 10 15
Ser Gln Val Asp Asn Val Ile Leu Gln Thr Gly Glu Ser Ala Ser Glu
20 25 30 35
Cys Phe Cys Leu Gln Cys Pro Ser Leu Gly Asn Ile Glu Gly Gly Val
40 45 50
Ala Thr Gly His Xaa
55

(2) INFORMATION FOR SEQ ID NO: 560:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2

seq LTCGPALVPRLWA/TC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 560:

```

Met Ser Trp Ser Gly Leu Leu His Gly Leu Asn Thr Ser Leu Thr Cys
-25                               -20                               -15

Gly Pro Ala Leu Val Pro Arg Leu Trp Ala Thr Cys Ser Met Ala Thr
-10                               -5                               1                               5

Leu Asn Gln Met His Arg Leu Gly Pro Pro Lys Arg Pro Pro Arg Lys
10                               15                               20

Leu Gly Pro Thr Glu Gly Arg Pro Gln Leu Lys Gly Val Val Leu Cys
25                               30                               35

Thr Phe Thr Arg Asn Arg
40

```

(2) INFORMATION FOR SEQ ID NO: 561:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq LEAFSQAISAIQA/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 561:

```

Met Ala Asp Val Ile Asn Val Ser Val Asn Leu Glu Ala Phe Ser Gln
-20                               -15                               -10

Ala Ile Ser Ala Ile Gln Ala Leu Arg Ser Ser Val Ser Arg Val Phe
-5                               1                               5

Asp Cys Leu Lys Asp Gly Met Arg Asn Lys Glu Thr Leu Glu Gly Arg
10                               15                               20                               25

Glu Lys Ala Phe Ile Ala His Phe Gln Asp Asn Leu His Ser Val Asn
30                               35                               40

Arg Asp Pro

```


(2) INFORMATION FOR SEQ ID NO: 562:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq RLLSSLLLTMSNN/NP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 562:

Met Asn Val Ile Asp His Val Arg Asp Met Ala Ala Ala Gly Leu His
-30 -25 -20

Ser Asn Val Arg Leu Leu Ser Ser Leu Leu Leu Thr Met Ser Asn Asn
-15 -10 -5

Asn Pro Glu Leu Phe Ser Pro Pro Gln Lys Tyr Gln Leu Leu Val Tyr
1 5 10 15

His Ala Asp Ser Leu Phe His Asp Lys Glu Tyr Arg Asn Ala Val Ser
20 25 30

Lys Tyr Thr Met Ala Leu Gln Gln Lys Lys Ala Leu Ser
35 40 45

(2) INFORMATION FOR SEQ ID NO: 563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq ACLAWTAVRPSAC/CH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 563:

Met Thr Ser Ala Cys Leu Ala Trp Thr Ala Val Arg Pro Ser Ala Cys
 -15 -10 -5

Cys His Pro Gln Ser Ala Asn Trp
 1 5

(2) INFORMATION FOR SEQ ID NO: 564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -55..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq VFGMSSSSGASNS/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 564:

Met Asn Gly Ser Arg Thr Leu Thr His Ser Ile Ser Asp Gly Gln Leu
 -55 -50 -45 -40

Gln Gly Gly Gln Ser Asn Ser Glu Leu Phe Gln Gln Glu Xaa Gln Thr
 -35 -30 -25

Ala Pro Ala Gln Val Pro Gln Gly Phe Asn Val Phe Gly Met Ser Ser
 -20 -15 -10

Ser Ser Gly Ala Ser Asn Ser Ala Pro His Leu Gly Phe His Leu Gly
 -5 1 5

Ser Lys Gly Thr Ser Ser Leu Ser Gln Gln Thr Pro Gly
 10 15 20

(2) INFORMATION FOR SEQ ID NO: 565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq FFLFLSFVLMYDG/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 565:

Met Leu Gly Phe Phe Leu Phe Leu Ser Phe Val Leu Met Tyr Asp Gly
-15 -10 -5

Leu Arg Leu Phe Gly Ile Leu Ser Thr Cys Arg Val His His Thr Met
1 5 10 15

Asn Gln Phe Leu Ile Asp Ile Ser Ser Phe Thr Ser Arg Val Arg
20 25 30

(2) INFORMATION FOR SEQ ID NO: 566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq SIKVLLQSALS LG/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 566:

Met Met Glu Glu Arg Ala Asn Leu Met His Met Met Lys Leu Ser Ile
-25 -20 -15

Lys Val Leu Leu Gln Ser Ala Leu Ser Leu Gly Arg Ser Leu Asp Ala
-10 -5 1 5

Asp His Ala Pro Leu Gln Gln Phe Phe Val Val Met Glu His Cys Ser
10 15 20

(2) INFORMATION FOR SEQ ID NO: 567:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids

(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -17..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.9
seq XIVSAALLAFVQT/HL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 567:

Met Glu Leu Glu Xaa Ile Val Ser Ala Ala Leu Leu Ala Phe Val Gln
-15 -10 -5
Thr His Leu Pro Glu Ala Asp Leu Ser Gly Leu Asp Glu Val Ile Phe
1 5 10 15
Ser Tyr Val Xaa Gly Val Leu Glu Asp Leu Gly Pro Ser Gly Pro Ser
20 25 30
Glu Glu Asn Phe Asp Met Glu Ala Phe Thr Glu Met Met Glu Ala Xaa
35 40 45
Val Pro Gly Phe Ala His Ile Pro Arg Gly Thr Ile Gly Xaa Met Met
50 55 60

(2) INFORMATION FOR SEQ ID NO: 568:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -26..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.9
seq SLIPLFXFIGTGA/TG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 568:

Met Leu Arg Gln Ile Ile Gly Gln Ala Lys Lys His Pro Ser Leu Ile
-25 -20 -15

Pro Leu Phe Xaa Phe Ile Gly Thr Gly Ala Thr Gly Ala Thr Leu Tyr
 -10 -5 1 5

Leu Leu Arg Leu Ala Leu Phe Asn Pro Xaa Val Cys Trp Asp Arg Xaa
 10 15 20

Asn Pro Glu Pro Trp Asn Xaa Leu Gly Pro Glu
 25 30

(2) INFORMATION FOR SEQ ID NO: 569:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -98..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq WTSLTCSLVVVDG/CG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 569:

Met Val Lys Glu Thr Gln Tyr Tyr Asp Ile Leu Gly Val Lys Pro Ser
 -95 -90 -85

Ala Ser Pro Glu Arg Ser Arg Arg Pro Ile Gly Ser Trp Arg Ser Ser
 -80 -75 -70

Thr Thr Arg Thr Arg Thr Arg Met Arg Ala Arg Ser Leu Asn Ser Tyr
 -65 -60 -55

Pro Arg His Met Lys Cys Phe Gln Ile Gln Arg Lys Gly Met Phe Met
 -50 -45 -40 -35

Thr Lys Ala Glu Ser Arg Gln Xaa Lys Lys Glu Ala Gln Ala Ala Pro
 -30 -25 -20

Ala Ser Leu His Pro Trp Thr Ser Leu Thr Cys Ser Leu Val Val Val
 -15 -10 -5

Asp Gly Cys Gly
 1

(2) INFORMATION FOR SEQ ID NO: 570:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -36..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq RALSTXLFGSIRG/AA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 570:

Met Ala Asn Leu Phe Ile Arg Lys Met Val Asn Pro Leu Leu Tyr Leu
-35 -30 -25

Ser Arg His Thr Val Lys Pro Arg Ala Leu Ser Thr Xaa Leu Phe Gly
-20 -15 -10 -5

Ser Ile Arg Gly Ala Ala Pro Val Ala Val Glu Pro Gly Ala Ala Val
1 5 10

Arg Ser Leu Leu Ser Pro Gly Leu Leu Pro His Leu Leu Pro Ala Leu
15 20 25

Gly Phe Lys Asn Lys Thr Val Leu Lys Lys Arg Cys Lys Asp Cys Tyr
30 35 40

Leu Val Lys Arg Arg Gly Arg Trp Tyr Val Tyr Cys Lys Thr His Pro
45 50 55 60

Arg His Lys Gln Arg His Met Xaa Thr Leu Ser Leu Gln Ser His Ala
65 70 75

Gln -

(2) INFORMATION FOR SEQ ID NO: 571:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -32..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.7
seq RIHLCQRSPGSQG/VR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 571:

Met Ala Ala Ala Ala Ala Ser Arg Gly Xaa Gly Ala Lys Leu Gly Leu
 -30 -25 -20

Arg Xaa Ile Arg Ile His Leu Cys Gln Arg Ser Pro Gly Ser Gln Gly
 -15 -10 -5

Val Arg Asp Phe Ile
 1 5

(2) INFORMATION FOR SEQ ID NO: 572:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -44..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq IALTLPMSLSRA/AG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 572:

Met Phe Pro Ser Cys Tyr Leu Cys Tyr Ser Leu Cys Gly Ser Ile Leu
 -40 -35 -30

Leu Ser Ile Phe Ser Ala Tyr Asn Arg Leu Ser Leu Met Leu Arg Ile
 -25 -20 -15

Ala Leu Thr Leu Ile Pro Ser Met Leu Ser Arg Ala Ala Gly Trp Cys
 -10 -5 1

Trp Tyr Lys Glu Pro Thr Gln Gln Phe Ser Tyr Leu Cys Leu Pro Cys
 5 10 15 20

Gly

(2) INFORMATION FOR SEQ ID NO: 573:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -60..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq QLXFLYFVCCIFQ/DV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 573:

Met Ser Thr Gln Xaa Gly Leu Ser Met His Ala His Pro Gln Ala Tyr
-60 -55 -50 -45
Thr Pro Phe Ile Tyr Leu His Ala Arg Lys Arg Arg Gly Glu Ile Gly
-40 -35 -30
Asp Ala Asp Ser Arg Phe Asn Asp Arg Tyr Ala His Lys Ser Ala Gln
-25 -20 -15
Leu Xaa Phe Leu Tyr Phe Val Cys Cys Ile Phe Gln Asp Val Tyr Tyr
-10 -5 1

Xaa
5

(2) INFORMATION FOR SEQ ID NO: 574:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -21..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq SSCSCSLISFTRG/DK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 574:

Met Lys His Phe Gln Asp Leu Pro Ser Ser Cys Ser Cys Ser Leu Ile
-20 -15 -10

Ser Phe Thr Arg Gly Asp Lys Tyr Phe Ala Tyr Asn Glu Glu Ile Phe
-5 1 5 10
Leu Val Tyr Asn Ala Asp Gln
15

(2) INFORMATION FOR SEQ ID NO: 575:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -62..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq SILGIISVPLSIG/YC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 575:

Met	Ser	Gln	Arg	Ser	Leu	Cys	Met	Asp	Thr	Ser	Leu	Asp	Val	Tyr	Arg
		-60					-55					-50			
Xaa	Leu	Ile	Glu	Leu	Asn	Tyr	Leu	Gly	Thr	Val	Ser	Leu	Thr	Lys	Cys
	-45					-40					-35				
Val	Leu	Pro	His	Met	Ile	Glu	Arg	Lys	Xaa	Xaa	Lys	Ile	Val	Thr	Val
-30					-25					-20					-15
Asn	Ser	Ile	Leu	Gly	Ile	Ile	Ser	Val	Pro	Leu	Ser	Ile	Gly	Tyr	Cys
				-10					-5					1	
Ala	Ser	Xaa	His	Ala	Leu	Xaa	Gly	Phe	Phe	Asn	Xaa	Leu	Arg	Thr	Xaa
		5					10					15			
Leu	Ala	Thr	Tyr	Pro	Gly	Ile	Ile	Val	Ser						
	20					25									

(2) INFORMATION FOR SEQ ID NO: 576:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -98..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.6
seq LALRTSWISSVCS/VT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 576:

Met Gly Gly Ser Gly Ser Arg Leu Ser Lys Glu Leu Leu Ala Glu Tyr
 -95 -90 -85

Gln Asp Leu Thr Phe Leu Thr Lys Gln Glu Ile Leu Leu Ala His Arg
 -80 -75 -70

Arg Phe Cys Glu Leu Leu Pro Gln Glu Gln Arg Xaa Xaa Ser Arg His
 -65 -60 -55

Phe Gly His Lys Cys Pro Ser Ser Arg Phe Ser Ala Phe Gln Ser Ser
 -50 -45 -40 -35

Arg Pro Thr Pro Ser Arg Ser Glu Ser Ala Gly Ser Ser Pro His Pro
 -30 -25 -20

Gln Pro Lys Thr Ala Leu Ala Leu Arg Thr Ser Trp Ile Ser Ser Val
 -15 -10 -5

Cys Ser Val Thr Gln Pro Arg Gln Thr Ser Ser Pro Ile Met Pro Ser
 1 5 10

Ala Ser Leu Thr Leu Met Met Thr
 15 20

(2) INFORMATION FOR SEQ ID NO: 577:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -28..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.6
seq PLSDSWALLPASA/GV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 577:

Met Trp Arg Leu Leu Ala Arg Ala Ser Ala Pro Leu Leu Arg Val Pro
 -25 -20 -15

Leu Ser Asp Ser Trp Ala Leu Leu Pro Ala Ser Ala Gly Val Lys Thr
 -10 -5 1

Leu Leu Pro Val Pro Ser Phe Glu Asp Val Ser Ile Pro Glu Lys Pro
 5 10 15 20

Lys Leu Leu

(2) INFORMATION FOR SEQ ID NO: 578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -114..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq ATFVTQALIQXYA/RI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 578:

Met Ala Asp His Val Gln Ser Leu Ala Gln Leu Glu Asn Leu Cys Lys
 -110 -105 -100

Gln Leu Tyr Glu Thr Thr Asp Thr Xaa Xaa Arg Ser Ser Xaa Ala Glu
 -95 -90 -85

Lys Ala Leu Val Glu Phe Thr Asn Ser Pro Asp Cys Leu Ser Lys Cys
 -80 -75 -70

Gln Leu Leu Leu Glu Arg Gly Ser Ser Ser Tyr Ser Gln Leu Leu Ala
 -65 -60 -55

Ala Thr Cys Leu Thr Lys Leu Val Ser Arg Thr Asn Asn Pro Leu Pro
 -50 -45 -40 -35

Leu Glu Gln Arg Ile Asp Ile Arg Asn Tyr Val Leu Asn Xaa Leu Ala
 -30 -25 -20

Thr Arg Pro Lys Leu Ala Thr Phe Val Thr Gln Ala Leu Ile Gln Xaa
 -15 -10 -5

Tyr Ala Arg Ile Thr Lys Leu Gly Trp Phe Asp
 1 5

(2) INFORMATION FOR SEQ ID NO: 579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -55..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq TCSVCCYLEFWLIA/IP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 579:

Met Ala Tyr His Gly Leu Thr Val Pro Leu Ile Val Met Ser Val Phe
-55 -50 -45 -40
Trp Gly Phe Val Gly Phe Leu Val Pro Trp Phe Ile Pro Lys Gly Pro
-35 -30 -25
Asn Arg Gly Val Ile Ile Thr Met Leu Val Thr Cys Ser Val Cys Cys
-20 -15 -10
Tyr Leu Phe Trp Leu Ile Ala Ile Pro Ala Trp
-5 1

(2) INFORMATION FOR SEQ ID NO: 580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -58..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq GGILMGSFQGTIA/GQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 580:

```

Met Ser Thr Gly Gln Leu Tyr Arg Met Glu Asp Ile Gly Arg Phe His
      -55                -50                -45

Ser Gln Gln Pro Gly Ser Leu Thr Pro Ser Ser Pro Thr Val Gly Glu
      -40                -35                -30

Ile Ile Tyr Asn Asn Thr Arg Asn Thr Leu Gly Trp Ile Gly Gly Ile
      -25                -20                -15

Leu Met Gly Ser Phe Gln Gly Thr Ile Ala Gly Gln Gly Thr Gly Ala
-10                -5                1                5

Thr Ser Ile Ser Glu Leu Cys Lys Gly Gln Glu Leu Glu Pro Ser Gly
      10                15                20

Ala Gly Leu Thr Val Ala Pro Pro Gln Ala Val Ser Leu Gln Gly Ser
      25                30                35

His Pro Ala Leu Ala Ala Thr Ala Phe Ser Leu Xaa Cys Pro Arg Gly
      40                45                50

Val Gln Xaa Leu Met Ile Ser Ile Ser Glu His Leu Phe Ile His Ala
55                60                65                70

```

(2) INFORMATION FOR SEQ ID NO: 581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (E) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq RWWCFHLQAEASA/HP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 581:

```

Met Gly Trp Gln Arg Trp Trp Cys Phe His Leu Gln Ala Glu Ala Ser
      -15                -10                -5

Ala His Pro Pro Gln Gly Leu Gln
  1                5

```

(2) INFORMATION FOR SEQ ID NO: 582:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Hypertrophic prostate
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -15..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.5
 seq VIFFACVVRVRDG/LP
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 582:

Met Ser Val Ile Phe Phe Ala Cys Val Val Arg Val Arg Asp Gly Leu
-15 -10 -5 1

Pro Leu Ser Ala Ser Thr Asp Phe Tyr His Thr Gln Asp Phe Leu Glu
 5 10 15

Trp Arg Arg Arg Leu Lys Ser Leu Ala Leu Arg Leu Lys
 20 25 30

(2) INFORMATION FOR SEQ ID NO: 583:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -16..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.5
 seq TALAAXTWLGWVG/VR
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 583:

Met Ala Val Thr Ala Leu Ala Ala Xaa Thr Trp Leu Gly Val Trp Gly
-15 -10 -5

Val Arg Thr Met Gln Ala Arg Gly Phe Gly Ser Asp Gln Ser Glu Asn
1 5 10 15

Val Asp Arg Gly Ala Gly Ser Ile Arg Glu Ala Gly Gly Ala Phe Gly
20 25 30

Xaa Arg Glu Gln Ala Glu Xaa Xaa Arg Tyr Phe
35 40

(2) INFORMATION FOR SEQ ID NO: 584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 12
seq FTLFLALIGGTSG/QY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 584:

Met Ser Leu Ser Ala Phe Thr Leu Phe Leu Ala Leu Ile Gly Gly Thr
-15 -10 -5

Ser Gly Gln Tyr Tyr Asp Tyr Asp Phe Pro Leu Ser Ile Tyr Gly Gln
1 5 10

Ser Ser Pro Asn Cys Ala Pro Glu Cys Asn Cys Pro Glu Ser Tyr Pro
15 20 25 30

Ser Ala Met Tyr Cys Asp Glu Leu
- 35

(2) INFORMATION FOR SEQ ID NO: 585:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -18..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 12
 seq FTLFLALIGGTSG/QY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 585:

Met Ser Leu Ser Ala Phe Thr Leu Phe Leu Ala Leu Ile Gly Gly Thr
 -15 -10 -5
 Ser Gly Gln Tyr Tyr Asp Trp
 1 5

(2) INFORMATION FOR SEQ ID NO: 586:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -18..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 12
 seq FTLFLALIGGTSG/QY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 586:

Met Ser Leu Ser Ala Phe Thr Leu Phe Leu Ala Leu Ile Gly Gly Thr
 -15 -10 -5
 Ser Gly Gln Tyr Tyr Asp Tyr Asp Phe Pro Leu Ser Ile Tyr Gly Gln
 1 5 10
 Ser Ser Pro Asn Cys Ala Pro Glu Cys Asn Cys Pro Glu Ser Tyr Pro
 15 20 25 30
 Ser Ala Met Tyr Cys Asp Glu Leu Lys Leu Lys Ser Val Pro Met Val
 35 40 45
 Pro Pro Gly Ile Lys Tyr Leu Tyr Leu Arg Asn Asn Gln Ile Asp His
 50 55 60
 Ile Asp Glu Lys Ala Phe Glu Asn Val Thr Asp Leu Gln Trp Leu Gly
 65 70 75

(2) INFORMATION FOR SEQ ID NO: 587:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.9
seq LLLLLLPFLLYMA/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 587:

```
Met Val Glu Leu Met Phe Pro Leu Leu Leu Leu Leu Pro Phe Leu
-20          -15          -10          -5

Leu Tyr Met Ala Ala Pro Gln Ile Arg Lys Met Leu Ser Ser Gly Val
          1          5          10

Cys Thr Ser Thr Val Gln Leu Pro Gly Lys Val Val Val Val Thr Gly
          15          20          25

Ala Asn Thr Gly Ile Gly Lys Glu Thr Ala Lys Glu Leu Ala Gln Arg
          30          35          40

Gly Ala Arg Val Tyr Xaa Ala Xaa Xaa Asp Val Glu Lys Gly Glu Leu
          45          50          55          60

Val Ala Xaa Glu Ile Gln Thr Thr Thr Gly Xaa Xaa Gln Val Leu Val
          65          70          75

Arg Xaa Leu Asp Leu Ser Asp Thr Lys Ser Ile Arg Ala Phe Ala
          80          85          90
```

(2) INFORMATION FOR SEQ ID NO: 588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.1

seq LLYLLVPALFCRA/GG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 588:

```

Met Trp Leu Leu Tyr Leu Leu Val Pro Ala Leu Phe Cys Arg Ala Gly
-15                -10                -5                1

Gly Ser Ile Pro Ile Pro Gln Lys Leu Phe Gly Glu Val Thr Ser Pro
          5                10                15

Leu Phe Pro Lys Pro Tyr Pro Asn Gly
      20                25

```

(2) INFORMATION FOR SEQ ID NO: 589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.7
seq LLFLVAGLLPSFP/AN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 589:

```

Met Lys Gln Ile Leu His Pro Ala Leu Glu Thr Thr Ala Met Thr Leu
-30                -25                -20

Phe Pro Val Leu Leu Phe Leu Val Ala Gly Leu Leu Pro Ser Phe Pro
-15                -10                -5

Ala Asn Glu Asp Lys Asp Pro Ala Phe Thr Ala Leu Leu Thr Thr Gln
 1                5                10                15

Thr Gln Val Gln Arg Glu Ile Val Asn Lys His Asn Glu Leu Arg Arg
      20                25                30

Ala Val Ser Pro Pro Ala Lys
      35

```

(2) INFORMATION FOR SEQ ID NO: 590:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -17..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 6.9
seq LFLTMLTLALVKS/QD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 590:

```
Met Leu Lys Ala Leu Phe Leu Thr Met Leu Thr Leu Ala Leu Val Lys
   -15                      -10                      -5
Ser Gln Asp Thr Glu Glu Thr Ile Thr Tyr Thr Gln Cys Thr Asp Gly
   1                      5                      10                      15
Tyr Glu Trp Asp Pro Val Arg Gln Gln Cys Lys Asp Ile Asp Glu Cys
   20                      25                      30
Asp Ile Val Pro Asp Ala Cys Lys Gly Gly Met Lys Cys Val Asn His
   35                      40                      45
Tyr Gly Gly Tyr Leu Cys Leu Pro Lys Thr Ala Gln Ile Ile Val Asn
   50                      55                      60
Asn Glu Gln Pro Gln Gln Glu Thr Gln Pro Ala Glu Gly Thr Ser Gly
   65                      70                      75
Ala Thr Thr Gly Val Val Ala Ala Xaa Ser Met Ala Thr Ser Xaa Val
   80                      85                      90                      95
Leu Xaa Gly Gly Gly Phe Val Ala Ser Ala Ala Ala Val Ala Gly Pro
   100                     105                     110
Glu Met Gln Thr Gly Arg Asn Asn Phe Val
   115                      120
```

(2) INFORMATION FOR SEQ ID NO: 591:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -22..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.9
 seq LLILWFHLDVCSS/IL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 591:

Met Glu Lys Asn Pro Leu Ala Ala Pro Leu Leu Ile Leu Trp Phe His
 -20 -15 -10
 Leu Asp Cys Val Ser Ser Ile Leu Asn Val Glu Gln Ser Pro Gln Ser
 -5 1 5 10
 Leu His Val Gln Glu Gly Asp Ser Thr Asn Phe Thr Cys Ser Phe Pro
 15 20 25
 Ser Ser Asn Phe Tyr Ala Leu His Trp Tyr Arg Trp Glu Thr Ala Lys
 30 35 40
 Ser Pro Glu Ala Val
 45

(2) INFORMATION FOR SEQ ID NO: 592:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -15..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.3
 seq VVTIVILLCFCKA/AE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 592:

Met Arg Val Val Thr Ile Val Ile Leu Leu Cys Phe Cys Lys Ala Ala
 -15 -10 -5 1
 Glu Leu Arg Lys Ala Ser Pro Gly Ser Val Arg Ser Arg Val Asn His
 5 10 15
 Gly Arg Ala Gly Gly
 20

(2) INFORMATION FOR SEQ ID NO: 593:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -90..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1
seq LLFVATLPFWTHY/LI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 593:

```

Met Asp Gln Phe Pro Glu Ser Val Thr Glu Asn Phe Glu Tyr Asp Asp
-90                               -85                               -80                               -75

Leu Ala Glu Ala Cys Tyr Ile Gly Asp Ile Val Val Phe Gly Thr Val
                               -70                               -65                               -60

Phe Leu Ser Ile Phe Tyr Ser Val Ile Phe Ala Ile Gly Leu Val Gly
                               -55                               -50                               -45

Asn Leu Leu Val Val Phe Ala Leu Thr Asn Ser Lys Lys Pro Lys Ser
                               -40                               -35                               -30

Val Thr Asp Ile Tyr Leu Leu Asn Leu Ala Leu Ser Asp Leu Leu Phe
-25                               -20                               -15

Val Ala Thr Leu Pro Phe Trp Thr His Tyr Leu Ile Asn Glu Lys Gly
-10                               -5                               1                               5

Leu His Asn Ala Met Cys
-                               10

```

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